Taylor, J. 09/524101

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Database

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| cgn2_6/ptodata/2/pna_VUSO6_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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APPLICANT: EXELIXIS, INC
TITLE OF INVENTION: Insect p53 Tumor Suppress;
FILE REFERENCE: Insect p53 sequences
CURRENT APPLICATION NUMBER: PCT/US00/06602A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: EX99-001
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
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; Mismatches
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CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 27
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TITLE OF INVENTION: Insect p53 Tumor Suppresible Reference: insect p53 Ex00-015

CURRENT APPLICATION NUMBER: US/09/524,101

CURRENT FILING DATE: 2000-03-13

PRIOR APPLICATION NUMBER: 09/268,969

PRIOR FILING DATE: 1999-03-16
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APPLICANT: Li, Peter W. D.
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLEUCLES ENCODING DROSOPHILA PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL000152
CURRENT APPLICATION NUMBER: US/60/167,217
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 23195
SOFTWARE: FastSeq for Windows Version 4.0
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LENGTH: 1241
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                    APPLICANT: Skupski, Marian
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS THAT SHOW
TITLE OF INVENTION: HIGH HOMOLOGY TO KNOWN HUMAN DISEASE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOO179
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CURRENT FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 579
SOFTWARE: FastSEQ for Windows Version 4.
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      Sequence 449, Application US/60171625 GENERAL INFORMATION:
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100.0%; Pr
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Matches 1230; Conser
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Sequence 449, A
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LENGTH: 1241
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US-60-191-637-22729; Application US/60191637
; Sequence 22729, Application US/60191637
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: NUCLEIC ACID DETECTION K
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000392
; CURRENT APPLICATION NUMBER: US/60/191,637
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 42660
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22729
; LENGTH: 1241
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; ORGANISM: DROSOPHILA
US-60-191-637-22729
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APPLICANT: Li, Peter, W.D.
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND
TITLE OF INVENTION: USES THEREOF.
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CURRENT APPLICATION NUMBER: US/60/191,681
CURRENT FILING DATE: 2000-03-23
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; Sequence 17941, Application US/60191681
; GENERAL INFORMATION:
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TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLEUCLES ENCODING DROSOPHILA PROTEINS, AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: CLOOO152 CURRENT APPLICATION NUMBER: US/60/167,217 CURRENT FILING DATE: 1999-11-24 NUMBER OF SEQ ID NOS: 23195 SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 5.1e-297;
; Mismatches 0;
               Sequence 22996, Application US/60167217 GENERAL INFORMATION: APPLICANT: Li, Peter W. D.
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LENGTH: 5453
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US-60-171-625-448

US-60-171-625-448

; Sequence 448, Application US/60171625
; GENERAL INFORMATION:
; APPLICANT: Skupski, Marian
TITLE OF INVENTION: HIGH HOMOLOGY TO KNOWN HUMAN DIS
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000179
; CURRENT FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 579
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 448
; LENGTH: 5453
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ORGANISM: DROSOPHILA
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Pred. No. 5.1e-297; 
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Best Local Similarity 87.4
Matches 1282; Conservative
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US-60-173-464-18651

Sequence 18651, Application US/60173464

GENERAL INFORMATION:

APPLICANT: Li, Peter W.D.

TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL000173

CURRENT APPLICATION NUMBER: US/60/173,464

CURRENT FILING DATE: 1999-12-29

NUMBER OF SEQ ID NOS: 30269

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 18651

LENGTH: 5453
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CURRENT APPLICATION NUMBER: US/60/191,681 CURRENT FILING DATE: 2000-03-23
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TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000392
CURRENT APPLICATION NUMBER: US/60/191,637
CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 42660
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 5454
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Pred. No. 5.1e-297;
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US-60-191-637-22728/c
; Sequence 22728, Application US/60191637
; GENERAL INFORMATION:
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Best Local Similarity
Matches 1282; Conser
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TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS
TITLE OF INVENTION: USES THEREOF.
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Conservative
SOFTWARE: FastSEQ for W: SEQ ID NO 17940
LENGTH: 5454
TYPE: DNA
                                             DROSOPHILA
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Best Local Similarity
Matches 1282; Conser
                                             ORGANISM: 0.60-191-681-
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CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09268969; GENERAL INFORMATION:
APPLICANT: Buchman, Andrew R.
APPLICANT: Platt, Darren M.
APPLICANT: Ollmann, Michael M.
APPLICANT: Young, Lynn M.
APPLICANT: Reegan, Kevin P.
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Д	σ ₀	gegttgageettgtaagtgaagataacaatacagategaacaggattatttaaetatea 39	
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a >-	76	acctggccttcaagttcgtctgccaaaactcgtgtatcggggggaaaagaaacttctt 827	
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₹ q	1006	attgctataaagacggaggacacggagagcaatgatagccgactgcgacgactccgcc 1065	
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1486	cgaaaagaaaacatttttatatttttgatagtatactgttgttaactgcagttctatgtg	1427	QY
4918		4859	QQ
1426	attagtccttgttcgtaaggcgtttaacggtgatattccccttttggcatgttcgatggc	1367	QY
4858	cetttgaaatgtgttgcatctgtggggtatactacatagctattagtatcttaagtttgt	4799	QC
1366	cctttgaaatgtgttgcatctgtggggtatactacatagctattagtatcttaagtttgt	1307	QY
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cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

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cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

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SUMMARIES

	Description	Sequence 203,	04,	1930,	1931,	193	1933,	1934,	3646, A	4152, A	15	564,	9081,	885,	1601,	451,		92	4998	10883	88, 🗚	612,	5, App	4487,	1049,	Sequence 5, Appli	e 1, Ap	32,
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88	-09-976-594-887	Ŋ		1.9	29.8	44		
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	-08-870-866-5	Ŋ	386	1.9	29.8	42		
Sequence 80, Appl	-886-055-8	Ŋ	957	1.9	30	41	O	
3612	388-906A-	ഗ	535	1.9	30	40		
Sequence 5376, Ap	-388-906A-537	ស	396	1.9	30	39		
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2354	-888-60	2	264	1.9	30.2	37	ပ	
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ALIGNMENTS

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1099 gattaccgtctggctattacgtgccccaataaggaatggctgctgcagagcatcgagggc 1158
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                                                                                                                                                                                                                      TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof FILE REFERENCE: 38-21(51847)B
CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
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Hinkle, Gregory J.
Huesing, Joseph E.
Krasomil-Osterfeld, Karina C.
                                   Sequence 203, Application US/09897516 GENERAL INFORMATION:
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Slater, Steven C.
Spiridonov, Sergei
                                                                      APPLICANT: Corbin, David R.
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; LOCATION: (705)..(1919)
US-09-897-516-203
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Krasomil-Osterfeld, Karina C.
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Hinkle, Gregory J.
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; GENERAL INFORMATION:
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Slater, Steven C.
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US-09-897-516-1931
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CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215, 161
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NUMBER OF SEQ ID NOS: 8409
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                Goldman, Barry S.
Hinkle, Gregory J.
Huesing, Joseph E.
Krasomil-Osterfeld, Karina
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APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp.
FILE REFERENCE: 38-21(51847)B
                                                                                                                                           TITLE OF INVENTION: Xenorhabdus sp. FILE REFERENCE: 38-21(51847)B CURRENT APPLICATION NUMBER: US/09/89 CURRENT FILING DATE: 2001-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Corbin, David R.
: Goldman, Barry S.
: Hinkle, Gregory J.
: Huesing, Joseph E.
: Krasomil-Osterfeld, k
: Malvar, Thomas M.
: Slater, Steven C.
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                                                                                  Malvar, Thomas M.
Slater, Steven C.
Spiridonov, Sergei
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PRIOR FILING DATE: 2000-06-30
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53.0%;
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David R
                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 8409
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                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (3103)..(6375)
S-09-897-516-204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (96)..(695)
US-09-897-516-1930
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LENGTH: 8093
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APPLICANT: APPLICANT: APPLICANT:

APPLICANT:

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Query Match Best Local

FEATURE:

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449 AAAGGACGACTGGGTAATATCGCCCCCCTGCAAGGGAGCCAGCACCAGATCCCCGGATGGT 390
                                  1159 atgattaaggaggcggcggctgaagtcctgc 1189
                                                  389 CTGATTATCGGGGCCTGAATGCTGTATTGC 359
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Best Local Similarity
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Best Local
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 Sequences And Uses
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TITLE OF INVENTION: Xenorhabdus sp. Genomerice Reference: 38-21(51847)B CURRENT APPLICATION NUMBER: US/09/897,516 CURRENT FILING DATE: 2001-06-29
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                                                             PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 1932
LENGTH: 8093
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Krasomil-Osterfeld, Karina APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei TITLE OF INVENTION: Xenorhabdus sp. Ge FILE REFERENCE: 38-21(51847)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1933, Application US/09897516 GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2001-
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SEQ ID NO 1933
LENGTH: 8093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Xenorhabdus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (2718)..(3014)
US-09-897-516-1933
                                                                                                                                                                             ^{\mathrm{ds}}
                                                                                                                                                                                                                           ; LOCATION: (2315)..(2641)
US-09-897-516-1932
                                                                                                                                                                           ORGANISM: Xenorhabdus
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Best Local Similarity
Matches 80; Conser
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LOCATION: (23
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                                                                                                                                                                                                                   APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
FILE REFERENCE: 38-21(51847)B
CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
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TITLE OF INVENTION: Constitutive rice promoters
FILE REFERENCE: 1360.026PRV
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Pred. No. 2.1;
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CURRENT FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 4708
SEQ ID NO 3646
LENGTH: 1811
                                                               APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Krasomil-Osterfeld, Karina APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
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                     Sequence 1934, Application US/09897516 GENERAL INFORMATION:
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SEQ ID NO 1934
LENGTH: 8093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Xenorhabdus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (6435)..(7883)
US-09-897-516-1934
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US-09-897-516-1934/c
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s-09-388-906A-15677/c
Sequence 15677, Application US/09388906A
GENERAL INFORMATION:
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US-09-680-959-564
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Best Local Similarity
Matches 63; Conser
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                                                                                                                                agcaatgatagccgagactgcgacgactccgccgcagagtggaacgtgtcgcggacacc
                                                                                                 gatggegattacegtetggetattaegtgeeceaataaggaatggetgetgeagageat
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  Indels
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
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   Mismatches
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FTWARE: FastSEQ for Windows Version 4.0
ID NO 4152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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US-09-815-242-4152

; Sequence 4152, Application US/09815242

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Trawick, John D.

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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US-09-815-242-4152
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Best Local
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APPLICANT: Havukkala, Ilkka
APPLICANT: Shenk, Michael Andrew
TITLE OF INVENTION: Polynucleotides Isolated From Plants and
TITLE OF INVENTION: Methods For Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Mutated Mammalian Cells and
TITLE OF INVENTION: Animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB Pred. No. 7.4; 0; Mismatches
                                                                             FILE REFERENCE: 11000.1013U
CURRENT APPLICATION NUMBER: US/09/388,906A
CURRENT FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 24843
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15677
LENGTH: 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: LEX-0051-USA CURRENT APPLICATION NUMBER: US/09/680,959 CURRENT FILING DATE: 2000-10-04 PRIOR APPLICATION NUMBER: US 60/157,651 PRIOR FILING DATE: 1999-10-04 NUMBER OF SEQ ID NOS: 574 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 564, Application US/09680959
GENERAL INFORMATION:
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
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; LOCATION: (1)...(261)
; OTHER INFORMATION: n = A,T,C or
US-09-388-906A-15677
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APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
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                                                                                                                                                                                                                                                                                                                                                                                                                  3673 GTTGTTTTTTTCCAAAGCAAAGGATACATTTTTTTTAAATCTACTGAACTAAAT 3614
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                                                                                                                                                                                                                                                                 Pred. No. 39;
; Mismatches
                                                                                        NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 399474.1
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PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
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APPLICATION NUMBER: US/60/235,711
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; Sequence 1601, Application US/09954456
; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-954-456-1601
                                                    ORGANISM: Homo sapiens
                                                                                                                             : NAME/KEY: unsure

: LOCATION: 2189, 2191,

: OTHER INFORMATION: a,

US-09-976-594-885
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96; Conserv
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LENGTH: 14800
SEQ ID NO 885
LENGTH: 4370
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                                      TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1262 tgccatgacttctgatctggtcgacaatctcccaggtatcagatacctttg
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Pred. No. 27;
0; Mismatches
                                                                                                                                                                                                                                                                                                              FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-33

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FASTSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
                                                                                                                                                                                                                          APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of
TITLE OF INVENTION: Prokaryotes
                                                                                             Sequence 9081, Application US/09815242 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 885, Application US/09976594 GENERAL INFORMATION:
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                                                                                                                                                     Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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illarity 55.9%;
Conservative (
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                                                                                                                                     : Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Furness, Michael APPLICANT: Buchbinder, Jen
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S-09-815-242-9081
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Matches 62; Conser
      299 ttcagtact 307
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                                                                                                                                                                                               6003 cacgetgegeageaaggageaggeegagetggaggeegegaggeageagetggegge 6062
                                                                                5883 gaggcagcggcaggtggaggaagagatcctggcgctgaaggcgaggttcgagaaggc 5942
                                                     gegggategeatecaagaegaaegeeageteaatageaagaagegeaagteegtgeegga 965
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0
 Length 14800;
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                                                                                                                                                                                                                                                                                                                         Sequence 451, Application US/09834975

Sequence 451, Application US/09834975

GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
APPLICANT: Bolt, Andrew
APPLICANT: Van Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REFERENCE: MRI-016B
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 451
LENGTH: 425
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                            Indels
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                           121;
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  DB
Score 32.4; DE Pred. No. 68; 0; Mismatches
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ch 2.1%;
(1 Similarity 46.5%;
105; Conservative
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; LOCATION: (1)...(425)
; OTHER INFORMATION: n =
US-09-834-975-451
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Description	Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 22998, A Sequence 450, App Sequence 18653, A Sequence 22730, A Sequence 17942, A
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APPLICANT: EXELIXIS, INC
TITLE OF INVENTION: Insect p53 Tumor Suppress; FILE REFERENCE: Insect p53 sequences
CURRENT APPLICATION NUMBER: PCT/US00/06602A; CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: EX99-001
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 7.4
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APPLICANT: Ollmann, Michael M.
APPLICANT: Young, Lynn M.
APPLICANT: Young, Lynn M.
APPLICANT: Demsky, Madelyn R.
APPLICANT: Keegan, Kevin P.
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOGASTER TUMOR TITLE OF INVENTION: SUPPRESSOR GENES AND USES THEREOF FILE REFERENCE: 7326-084
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TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins FILE REFERENCE: insect p53 EX00-015
CURRENT APPLICATION NUMBER: US/09/524,101
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 09/268,969
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 2000-02-23
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                    Application US/09268969
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SOFTWARE: PatentIn version 3.0
                                                                    APPLICANT: Buchman, Andrew R.
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385; Conser
                      Sequence 2, Applications: GENERAL INFORMATION:
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US-09-268-969-2
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TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLEUCLES ENCODING DROSOPHILA PROTEINS,
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL000152
CURRENT APPLICATION NUMBER: US/60/167,217
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 23195
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22998
LENGTH: 381
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Pred. No. 7.4
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Pred. No. 2.
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IS-60-167-217-22998
Sequence 22998, Application US/60167217
GENERAL INFORMATION:
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; ORGANISM: Drosophila melanogaster
US-09-524-101-2
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SEQ ID NO 2
LENGTH: 385
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Sequence 450, Application US/60171625

GENERAL INFORMATION:
APPLICANT: Skupski, Marian
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS THAT SHOW
TITLE OF INVENTION: HIGH HOMOLOGY TO KNOWN HUMAN DISEASE I
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Pred. No. 2.4e-188;
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CURRENT FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 579
SOFTWARE: FastSEQ for Windows Version 4.
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TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL000173

CURRENT APPLICATION NUMBER: US/60/173,464

CURRENT FILING DATE: 1999-12-29

NUMBER OF SEQ ID NOS: 30269

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 18653

LENGTH: 381
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TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL0000392
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Pred. No. 2.4e
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CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 42660
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22730
LENGTH: 381
                      Sequence 18653, Application US/60173464 GENERAL INFORMATION:
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nilarity 99.5%;
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; ORGANISM: Drosophila
US-60-173-464-18653
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Les 378; Conserver
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APPLICANT: Li, Peter, W.D.
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND
TITLE OF INVENTION: USES THEREOF.
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  Score 1973; DB 24;
Pred. No. 2.4e-188;
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CURRENT APPLICATION NUMBER: US/60/191,681
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; Sequence 17942, Application US/60191681
; GENERAL INFORMATION:
; APPLICANT: Li, Peter, W.D.
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CURRENT APPLICATION NUMBER: PCT/US00/06602A CURRENT FILING DATE: 2000-03-13 PRIOR APPLICATION NUMBER: EX99-001 PRIOR FILING DATE: 1999-03-16
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nes 122;
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Pred. No. 1.
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                                                                                                                                                                                                                                              TITLE OF INVENTION: Insect p53 Tumor String Reference: Insect p53 sequences CURRENT APPLICATION NUMBER: PCT/US00/01CURRENT FILING DATE: 2000-03-15 EARLIER APPLICATION NUMBER: EX99-001 EARLIER FILING DATE: 1999-03-16 NUMBER OF SEQ ID NOS: 22 SOFTWARE: Patentin Ver. 2.1
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APPLICANT: EXELIXIS, INC
TITLE OF INVENTION: Insect p53 Tumor FILE REFERENCE: Insect p53 sequences
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TITLE OF INVENTION: Inse
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TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins FILE REFERENCE: insect p53 EX00-015
CURRENT APPLICATION NUMBER: US/09/524,101
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 09/268,969
PRIOR FILING DATE: 1999-03-16
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                                                                                            DB 1;
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ORGANISM: Leptinotarsa decemlineata
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TESNDSRDCDDSAAEWNVSRTPDGD-----YRLAITCPNKEWLLQSIEGMIKEAAAEVLR
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Pred. No. 2.3e-15;
7; Mismatches 124;
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TITLE OF INVENTION: Insect p53 Tumor Suppress;
FILE REFERENCE: Insect p53 sequences
CURRENT APPLICATION NUMBER: PCT/US00/06602
CURRENT FILING DATE: 2000-03-15
EARLIER APPLICATION NUMBER: EX99-001
EARLIER FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application PC/TUS0006602 GENERAL INFORMATION:
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ENGTH: 350
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- VPQGSSDNKIFALNIHIPGKKNYLQALKMCQDMLANEILK 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins FILE REFERENCE: Insect p53 sequences
CURRENT APPLICATION NUMBER: PCT/US00/06602A
CURRENT FILING DATE: 2000-03-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
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CURRENT APPLICATION NUMBER: US/09/524,101
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 09/268,969
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/184,373
                                                                                                                                                                                         Sequence 6, Application PC/TUS0006602A GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC
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PRIOR FILING DATE: 1999-03-16
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                                                                                                                                                Query Match
12.3%; Score 247.5; DB 19;
Best Local Similarity 24.2%; Pred. No. 2.3e-15;
Matches 88; Conservative 67; Mismatches 124;
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Tribolium castaneum
US-09-524-101-6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	equence 340, Ap	equence 344, Ap	ence 339, Ap	ence 342, Ap	2, Ap	e 341, Ap	343, Ap	equence 338, Ap	15, App	16, App	15, App	16, App	equence 17, App	ednence	equence 17, App	1035, A	42, App	equence 3, Appl	App	2811,	equence 6135, A	e 28, App	e 34, App	e 5408, A	2490,	e 11825,	Sequence 147, App
	QI	US-09-850-716A-34	-850-716A-	-09-850-716A-	-09-850-716A-3	-850-716A-15	-09-850-716A-34	-09-850-716A-3	-09-850-716A-33	-09-609-360C-1	-09-609-360C-1	-345-473E-1	-09-345-473E-1	-09-609-360C-1	~	-09-816-028A-1	09-976-594-10	9369-4	-US01-31656-	-US01-17103-1	-815-242-12	-897-516-613	S-09-848-909-2	-848-90	-09-815-242-540	-09-815-242-1249	15-242-118	S-09-974-298-14
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US-09-659-287A-2 US-09-976-594-296	-09-815-242-1	-09-803-671B-2	US-09-897-516-6293	7-516-568	US-09-897-516-6662	ا جم	US-09-981-353-95	US-09-973-278-386	-515-1	US-09-969-515-6	US-09-815-242-13515	US-09-969-515-10	US-09-969-515-4	US-09-969-515-8	US-09-969-515-2	US-09-897-516-5947
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28	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT US-09-850-716A-340 ; Sequence 340, App; ; GENERAL INFORMATI; ; APPLICANT: Relos; ; APPLICANT: McNe; ; TITLE OF INVENTI; ; TITLE OF INVENTI; ; TITLE OF INVENTI; ; TITLE OF INVENTI; ; CURRENT APPLICAT; ; CURRENT APPLICAT; ; CURRENT FILING D ; SOFTWARE: FASTSE; ; SOFTWARE: PRT ; ORGANISM: HOMO US-09-850-716A-340 QV	16A-340 340, Application US/09850716A NFORMATION: TE Kalos, Michael D. TT: McNeill, Patricia D. TT: Retter, Marc W. TY: Retter, Marc W. TY: NOWENTION: COMPOSITIONS AND METHODS FOR THE THERAPY INVENTION: AND DIAGNOSIS OF LUNG CANCER FRENCE: 210121.455C15 APPLICATION NUMBER: US/09/850,716A APPLICATION NUMBER: US/09/850,716A FILING DATE: 2001-05-07 FEST ID NOS: 440 THE THANK THE THERAPY FILING SALOR WINDOWS Version 3.0 THE TABLES OF WINDOWS VERSION 3.0 THE TABLES OF THE	ch 1 Similarity 22.2%; Pred. No. 2.5e-10; 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;	OPMSWHKESTDSEDDST-EVDIKEDIPKTVEVSGSELTTEPMAFLQGLNSGNLMOFSQQS 63 : : : :: : : : OPIDINEVDEPSEDGATNKIEISMDCIRMODSDL-SDPMWPOYTNIG 76		:	GGYCFSMVLDEPPKSLWMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF 145	PHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP-QGAVIRAMPVY 192	SNDVSAPVVRCQNHLSVEPLTANNAKMRESLLRSENPNSVYCGNAQGKGISERF 199	KAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQ 245	SVVVPLNMSRSVTRSGLTRQTLAFKFVCQNSCIGRKETSLVFCLEKACGDIVGQHVI 256		HVKICTCPKRDRIQDERQLNSKKRKSVPEAAEEDEPSK 294	ARICACPGRDRKADEDSIRKQQVSDSTKNGDGTK 336
RESULT US-09-850- Sequence GENERAL REPLICAL RAPPLICAL RAPPLICAL RITLE OF TITLE OF TI	716A-340 340, Ap 340, Ap INFORMAT NT: Kalo NT: Ret FINVENT FIRENCE: APPLICA FILING FILING O 340 : 448 : 448 SM: HOMC	Sim 5;	QPMSWHKI	VLREMML	: LLNSM	GGYCFSM	GPHSFDV	SNDVS	KKAEHVTI	SVVVPLN	SVLVPY-	HVKICTCI	EARICACI
Sister Constitution of the	JLT 1 99-850- equence energh APPLICA APPLICA APPLICA APPLICA TILE O FITLE O	uery Ma est Loc atches						146	193	200	246		
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Indels

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31 QPIDLNFVDEPSEDGATNKIEISMD---CIRMQDSDL-SDPM--
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 Mismatches 124;
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4.6e-10;
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Pred. No. 4.6e-
59; Mismatches
                                                                                             VLREMMLQDIQIQ ---ANTLPKLENH----
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 59;
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'5; Conservative
   Conservative
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                   Length 516;
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GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455c15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
                                                                                                                                                                                                                                                                                                                                                                  124;
                                                                                                                                                                                                                                                                                                                                                                                                                   186; DB 5;
No. 4.2e-10;
                                                                                                           TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCELLE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 3.1e-10
9; Mismatches 12
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SOFTWARE: FastSEQ for Windows Version
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Pred.
                                 Sequence 344, Application US/09850716A GENERAL INFORMATION:
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                                                              APPLICANT: Kalos, Michael D. APPLICANT: McNeill, Patricia D. APPLICANT: Retter, Marc W. TITLE OF INVENTION: COMPOSITIONS TITLE OF INVENTION: AND DIAGNOSI
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Best Local Similarity
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ORGANISM: Homo :
S-09-850-716A-339
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                  US-09-850-716A-344
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ENGTH: 641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 SVLVPY----EPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCF 301
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QPMSWHKESTDSEDDST-EVDIKEDIPKTVEVSGSELTTEPMAFLQGLNSGNLMQFSQQS 63
                                                                                -- WPOYTNLG 76
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                  Sequence 343, Application US/09850716A GENERAL INFORMATION:
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B≈st Local Similarity
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ENGTH: 461
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LENGTH: 586
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APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455c15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 1.7e-09;
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APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR 1
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
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llarity 25.6%; Pred. No. 1e-(
Conservative 38; Mismatches
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                                                                                                     Sequence 152, Application US/09850716A GENERAL INFORMATION:
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EPLTANNAKMRESLLRSENPNSVYCGNAQGKGISE----RFSVVVPLNMSRSVTRSGLTR 218
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                                     206 TTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADE---
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APPLICANT: Ralos, Michael D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Fast: 20 for Windows Version 3.0
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
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CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Meyers, Rachel
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                                                                                                                                                                                                                                                                                                                                                                                       -----GNSHAQYVEDPITGRQSVLVPY---EPPQVGTEF
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                                                                                                                                   Length 586;
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0.074;
                                                                                                                                                                                                                                          105 WMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF-
                                                                                                             Score 178; DB 5,
No. 2.1e-09
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                                                                                                                                                              ed. No. 2.16
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/609,360C CURRENT FILING DATE: 2000-06-30 PRIOR APPLICATION NUMBER: 09/562,480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/09609360C; GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
APPLICANT: Meyers, Rachel
APPLICANT: Williamson, Mark
TITLE OF INVENTION: Novel Kinases and
FILE REFERENCE: MPI1999-096CP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                   38;
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                                                                                                                                8.98;
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PRIOR FILING DATE: 1999-06-30
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Best Local Similarity
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; TYPE: PRT
; ORGANISM: HOMO
US-09-850-716A-338
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TRSRTK-
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Best Local
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268 RIQDERQLNSKKRKSVPEAAEEDEPSKVRRCIAIKTEDTESNDSRDCDDSAAEWNVSRTP 327
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                                                         ---AKTAETEEGTS-DOKNKRFSWE-KESE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Williamson, Mark
TITLE OF INVENTION: Novel Kinases and Uses Thereof
FILE REFERENCE: MPI1999-096CP2
CURRENT APPLICATION NUMBER: US/09/609,360C
CURRENT FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.9%; Score 98.5; DB larity 19.0%; Pred. No. 0.074; Conservative 57; Mismatches 1
                                                                                                                            328 DGDYRLAITCPNKEWLLQSIEGMIKEAAAEVLRN----
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PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                          --RAY 382
                                                                                                                                                                                                                                                                                                                        378 FPRMDEFKRHIEILGRLKHPNLVPLRAY 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/09609360C GENERAL INFORMATION:
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                                                             274 RSKSKRE--ERRSKRVAESKE----
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Williamson, Mark
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                                                                                                                                                                                                                                                                                                                                                 82
                                                                                                                                                                                                                                                                                                                     SQPMSWHKESTDSEDDSTEVDIKEDIPKTVEVSGSELTTEPMAFLQGLNSGNLMQFSQQS 63
                                                                                                                                                                                                                                                                                                                                    --EGVKKCMKGRVSKLVLENLNLSGSLNGKSLNQLDQLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SA--PVVRCQNHLSVEPLTANNAKMRESLLRSENPNSVYCGNAQGKGISERFSVVVPLNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --LIGIISGSI------CGGILILLLTFLLICLLWRRK
                                                                                                                                                                                                                                                                                                                                                                            --KLENHNIGGYCFSMVLDEPPKSLW-
                                                                                                                                                                                                                                                                                      151;
                                                                                                                                                                                                                                                           Length 645;
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                        Score 98.5; Db J. No. 0.074;
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hodge, Martin
TITLE OF INVENTION: Novel Kinases and Uses
FILE REFERENCE: 35800/183781
CURRENT APPLICATION NUMBER: US/09/345,473E
                                                                  TITLE OF INVENTION: Novel Kinases and Uses FILE REFERENCE: 35800/183781
CURRENT APPLICATION NUMBER: US/09/345,473E
CURRENT FILING DATE: 1999-06~30
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGDYRLAITCPNKEWLLQSIEGMIKEAAAEVLRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGHIPPTQALNRFNESSFTDNIALCGDQIQNS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Version 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/09345473E GENERAL INFORMATION:
                         Application US/09345473E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --RAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FPRMDEFKRHIEILGRLKHPNLVPLRAY
                                                                                                                                                                                                                                                                                     57;
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                                                                                                                                                                                                    Arabidopsis thaliana
                                                                                                                                                                                                                                                            4.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 RSKSKRE--ERRSKRVAESKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - PNQENLRRHANKLLSLKK -
                                                                                                                                                                                                                                                                                                                                                                               VLREMMLQDIQIQANTLP--
                                                                                                                                                                                                                                                                                        Conservative
                                                        APPLICANT: Hodge, Martin
                                                                                                                                                                                                                                                                           Similarity
                            Sequence 15, Applica GENERAL INFORMATION:
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US-09-345-473E-16
RESULT 11
US-09-345-473E-15
                                                                                                                                                                                                                 US-09-345-473E-15
                                                                                                                          NUMBER
SOFTWARE: Faster
FO ID NO 15
                                                                                                                                                                                                                                                                                                                                                 TDPCNW
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Best Local 3
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318 EGSVGTLVFLGRDITVVRYTMDDLLKASAETLGRGTLGSTYKAVMESGFIITVKRLKDAG 377
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                                                                                                                                                                                                       --KLENHNIGGYCFSMVLDEPPKSLW--- 105
                                                                                                                                                                                                                                     : |:|
-SFKGNSLSGSIPNLSGLVNLKSLYLNDNNFSG-----EFPESLTSLH 126
                                                                                                                                                                                                                                                                                                          -MYSIPLNKLYIRMNKAFNVDVQ---FKSKMPIQPLN---LRVFLCFSNDV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 SCHIPPTQALNRFNESSFTDNIALCGDQIQNS-----CNDTTGITSTPSAKPAIPVAK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --LIGIISGSI-----CGGILILLLTFLLICLLWRRK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----AKTAETEEGTS-DQKNKRFSWE-KESE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                  4 SQPMSWHKESTDSEDDSTEVDIKEDIPKTVEVSGSELTTEPMAFLQGLNSGNLMQFSQQS 63
                                                                                                                                  SRSVTRSGLTRQTLAFKFVCQNSCIGRKETSLVFCLEKACGDIVGQHVIHVKICTCPKRD
                                                                                                                                                                                                                                                                                                                                                                                                          SA--PVVRCQNHLSVEPLTANNAKMRESILRSENPNSVYCGNAQGKGISERFSVVVPLNM
                                                                                                                                                                                                                                                                                                                                          127 RLKTVVLSRNRFSGKIPSSLLRLSRLYTFYVQDNLFSGSIP--PLNQATLRFFNVSNNQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 RIQDERQLNSKKRKSVPEAAEEDEPSKVRRCIAIKTEDTESNDSRDCDDSAAEWNVSRTP
 Length 645;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Meyers, Rachel
APPLICANT: Williamson, Mark
TITLE OF INVENTION: Novel Kinases and Uses Thereof
FILE REFERENCE: MPI1999-096CP2
CURRENT APPLICATION NUMBER: US/09/609,360C
CURRENT FILING DATE: 2000-06-30
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                                                  155;
DB 5;
4.9%; Score 98.5; DB 19.0%; Pred. No. 0.074; ive 57; Mismatches 1
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20.0%; Pred. No. 0.12;
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SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-609-360C-17
; Sequence 17, Application US/09609360C
; GENERAL INFORMATION:
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                                           57;
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PRIOR APPLICATION NUMBER: 09/3
PRIOR FILING DATE: 1999-06-30
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                                                  Conservative
                                                                                                                                                                                                       64 VLREMMLODIQIQANTLP --
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| 85; Conserv
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LENGTH: 604
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142
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                          MPIQPLN---LRVFLCFSNDVSAPVVRCQNGLUVEPLTANNAKMRESLLRSENPNSVYCG 188
                                                      -SFTGNVALCG 187
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--SFKANSLSGSIPNLSGLVNLKSVY 85
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GS
                                                                               NAQGKGISERFSVVVPLNMSRSVTRSGLTRQTLAFKFVCQNSCIGRKETSLVFCLEKACG
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LNDNNFSGDFPESLTSLHRLKTIFLSG---NRLSGRIPSSLLRLSRLYTLNVEDNLFT
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                                                                                                                                                                                                                                                  -RNPNQENLRRHANKLLSLKK--
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Pred. No. 0.12;
5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hodge, Martin
TITLE OF INVENTION: Novel Kinases and Uses Th
FILE REFERENCE: 35800/183781
CURRENT APPLICATION NUMBER: US/09/345,473E
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKLVLEYLNLTGSLNEKSLNQLDQLRVL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.8%; SC
20.0%; Pre
                                              : | | | | | | : | : | : | : | : | IP--PLNQTSLRYFNVSNNKLSGQI-
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US-09-345-473E-17
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APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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llarity 22.5%; Pred. No. 0.14;
Conservative 31; Mismatches 62;
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                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/118,213
                                                                                                                                                                                                                                                                                    US 09/495,406
                  Sequence 17, Application US/09816028A
GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
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                                                                                                                                                                       FILE REFERENCE: 019633-000111US
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2000-01
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver.
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Best Local Similarity
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US-09-816-028A-17
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LENGTH: 347
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updates/sec US-09-524-101-2 2008 1 MYISQPMSWHKESTDSEDDS......NLRRHANKLLSLKKRAYELP 385 ; Search time 50.08 Seconds (without alignments)
466.059 Million cell update 2001, 15:03:33 November 16, score: Scoring table: Sequence: Title: Perfect Run on:

412676 seqs, 60623988 residues Gapext 0.5 BLOSUM62 Gapop 10.0 Searched:

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hits satisfying chosen parameters

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Total number

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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printed, Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being primand is derived by analysis of the total score distribution.

SUMMAKIES		ID Description		AAB00120 CPBp53 tumour supp	AAB00121 TRIB-Ap53 tumour's	AAY50999 Human p73 proteir	AAW36190 Human p53 tumour s	p7	AAW30661 Human NBS-1 alpha		AAY44634 Human p73 alpha sp	Monkey	
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		Length	385	354	350	636	499	499	635	636	636	499	
ď	Onorg	Match Length DB	100.0	15.0	12.3	6.7	5.0	9.5	9.5	9.5	9.5	9,5	
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ALIGNMENTS

DMp53 tumour suppressor polypeptide. AAB00119 standard; Protein; 385 AA. (first entry) 08-FEB-2001 AAB00119; **AAB**00119 RESULT

p53; tumour suppressor gene; insect; phenotype; metazoa; invertebrate; screening; pharmaceutical; pesiticide; mis-expression; mutation; modulation.

Drosophila melanogaster.

16-MAR-1999; 99US-0268969. 23-FEB-2000; 2000US-0184373. 13-MAR-2000; 2000WO-US06602. WO200055178-A1. 21-SEP-2000.

Keegan KP; Platt DM, Ollman MM, Young LM, Demsky MR, Kopczynski C, Larson JS, Robertson SA; Buchman AR, Friedman L,

(EXEL-) EXELIXIS INC.

WPI; 2000-638178/61. N-PSDB; AAA53973.

Novel p53 tumor suppressor gene encoding a protein useful for

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                                                                                 metazoan invertebrate organisms, such as insects and worms, or metazoan invertebrate organisms, such as insects and worms, or cultured cells, resulting in p53 expression or mis-expression. The tumour suppressor genes, a p53 polypeptide or genetically modified organisms or cells are used in screening assays to identify compounds or molecules, preferably a pharmaceutical agent or a pesticide, that modulates p53 activity. The genetically modified organisms or cells are also useful for studying p53 activity by detecting the phenotype caused by the expression or mis-expression of the p53 protein in the insect. The method additionally comprises observing a second insect having the same genetic modification as the previous one, which causes the expression or mis-expression of the p53 protein, where the second animal additionally comprises a mutation in a desired gene and differences between the phenotype of the first and second identifies the desired gene as capable of modifying the function of the gene cells are also useful for identifying other genes modulating the tention of, or interaction with the p53 gene.
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invertebrate; screening; pharmaceutical; pesiticide; mis-expression;
mutation; modulation.
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Pred. No. 3.9e-203;
Mismatches 0;
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                                            Claim 14; Page 70-71; 98pp; English
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metazoan invertebrate organisms, such as insects and worms, or cultured cells, resulting in p53 sepression or mis-expression. The tumour suppressor genes, a p53 polypeptide or genetically modified organisms or cells are used in screening assays to identify compounds or molecules, preferably a pharmaceutical agent or a pesticide, that modulates p53 activity. The genetically modified organisms or cells are also useful for studying p53 activity by detecting the phenotype caused by the expression or mis-expression of the p53 protein in the insect. The method additionally comprises observing a second insect having the same genetic modification as the previous one, which causes the expression or mis-expression of the p53 protein, where the second animal additionally comprises a mutation in a desired gene and differences between the phenotype of the first and second identifies the desired gene as capable of modifying the function of the gene cells are also useful for identifying other genes modulating the function of, or interaction with the p53 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insect p53 tumour suppressor genes can be used to genetically modify
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C, Larson JS, Robertson SA;
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Similarity 28.5%; Pred. No. 5.7e-23;
3; Conservative 60; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 MAFLQGLNSGNLMQFSQQSVLREMMLQDI - - - QIQAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; Page 73-74; 98pp; English.
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                                                                                                                                                                                        2000US-0184373
                                                                                                                          2000WO-US06602
                                                                                                                                                                    99us-0268969
                                                                                                                                                                                                                                                                          Platt DM, Oll
Kopczynski C,
Leptinotarsa decemlineata
                                                                                                                                                                                                                                  (EXEL-) EXELIXIS INC.
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N-PSDB; AAA53974.
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                                        WO200055178-A1.
                                                                                                                       13-MAR-2000;
                                                                                                                                                             16-MAR-1999;
                                                                                                                                                                                       23-FEB-2000;
                                                                                1-SEP-2000.
                                                                                                                                                                                                                                                                          Buchman AR,
Friedman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 28pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human p73 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Keegan KP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        caused by the expression or mis-expression of the p53 protein in the insect. The method additionally comprises observing a second insect having the same genetic modification as the previous one, which causes the expression or mis-expression of the p53 protein, where the second animal additionally comprises a mutation in a desired gene and differences between the phenotype of the first and second identifies the desired gene as capable of modifying the function of the gene encoding the p53 protein. The genetically modified organisms or cells are also useful for identifying other genes modulating the function of, or interaction with the p53 gene.
                     re 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                        ippressor gene; insect; phenotype; metazoa;
screening; pharmaceutical; pesiticide; mis-expres
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th as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           el p53 tumor suppressor gene encoding a protein useful for
etically modifying metazoan invertebrate organisms, such
screening compounds of pharmaceutical use or a pesticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Young LM, Demsky MR,
S, Robertson SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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  TRIB-Ap53 tumour suppressor polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ollman MM, You
C, Larson JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98pp; English
                                                                                                                                                                                                                   standard; Protein; 350 AA
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2000US-0184373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Platt DM,
Kopczynski
                                                                                                                                                                                                                                                                                                                                                                                             p53; tumour suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                   mutation; modulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EXEL-) EXELIXIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tribolium castaneum
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N-PSDB; AAA53975.
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Best Local Similarity
Matches 88; Conserv
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WO200055178-A1

13-MAR-2000;

21-SEP-2000

16-MAR-1999; 23-FEB-2000;

AR,

Friedman L,

invertebrate;

08-FEB-2001

AAB00121;

AAB00121

AAB001

352

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351

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AA 355

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Οy

Claim 14; Page

Sequence

Novel p53 to genetically

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detect presence or absence of human chromosome 3q27 or murine chromosome 16, or their fragments, by hybridization. Also, (I) is used as a tumor suppressor, particularly in tumors where an alteration in the wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encodes a protein, (II), involved in control of the cell cycle and apoptosis, i.e. (II) is a tumor suppressor protein which belongs to the p53 family. (I), and the polypeptide (II) encoded by it, are used (a) to detect (I) in biological samples, specifically angiogenic tumor tissue, including (I) sequences that have a homozygotic deletion and (b) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel KET-encoding nucleic acid (I) and its fragments, variants and mutants which has anticancer activity. (I) encodes a protein, (II), involved in control of the cell cycle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New KET-encoding nucleic acid and related proteins, for diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KET; anticancer; cell cycle; apoptosis; tumor suppressor; p53 family; p53 family; angiogenic; cytotoxic; cancer; human; p73.
                                                                                                    KLENHNIGGYCFSMVLD-EPPKSLWMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLR 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -kntgtrlnivlplahpqvgedvvke-----ffqfvcknscplgmnrrpidvvftled 231
                                                                                                                                                                                                                                                                       141 VFLCFS-----NDVSAPVVRCQNHLSVEPLTANNAKMR----ESLLRSENPNSVYCGNAQ 191
                                                                                                                                                                                                                                                                                                                                 127 atpvfsqtqhfqdl---vhrcvghr--hpqdqsnkgvaphifqhiirctndnalyfgd--
lkddvgrimhennvhlvnd-----dgeeekysneanytesifppdqptnlgteeyp
                                                                                                                                                                                                                                                                                                                                                                                                                                             306 TESNDSRDCDDSAAEWNVSRTPDGD----YRLAITCPNKEWLLQSIEGMIKEAAAEVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 ACGDIVGQHVIHVKICTCPKRDRIQDERQLNSKKRKSVPEAAEEDEPSKVRRCIAIKTED
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risk of
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                                                                                                                                                                --PPKSL 104
                                                                                                                                                                                                        WMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQP-LNLRVFLCF--SNDVSAPVVRCQNHLS 161
                                                                                                     Gaps
                                                                                                                                   suppressor gene;
ir; neuroblastoma;
                                                                                                                                                                                                                                              VEPLTANNAKMRESLLRSENPN-SVYCGNAQGKGISERFSVVVI'LNMSRSVTRSGLTRQT
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identified. (I) and (II) may also be use cytotoxic agents and for predicting the sequence represents the human p73 proteiof the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide(s) encoded by the SR-p70 tumour suppressor gene and related nucleic acid, useful for diagnosis and treatment of
                                                                                                                        EDDSTEVDIKEDIPKTVEVSGSELTTEPMAFLQGLNSGNLMQFSQQSVLREMMLQ-
                                                                                                                                                                                                                                                                                       LAFKFVCQNSCIG - - - RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDE -
                                                                                 Length 636;
                                                                                                                                                               -DIQIQANTLPKLENHNIGGYCFSMVLDE-
                                                                                                     Indels
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                                                                                                                                                                                                                                                           -11;
142;
                                                                                Score 194; DB 21
Pred. No. 2.6e-11
}; Mismatches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SR-p70; human; transcription factor; p53; to homology; differential splicing; diagnosis;
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                                                                                                   48;
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                                                                                9.7%;
ilarity 23.9%;
Conservative 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy; apoptosis.
p53 allele has not been development of specific developing cancer. This described in the method
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                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                 Query Match
Best Local Similarity
Matches 78; Conser
                                                    AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAW36190
                                                    Sequence
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This is the amino acid sequence of the human protein SR-p70b. SR-p70 are transcription factors which may control the activity of p53-regulated genes, and are expressed by tumour suppressor genes related to the p53 gene family. The gene sequence was isolated from the human neuroblastoma cell line SK-N-SH, using primers AAV01515 and AAV01518. The SR-p70b gene sequence contains a 94 bp deletion between bases 1516-1517 as compared to the SR-p70a sequence (AAV01498). This deletion causes a reading frame shift resulting in the generation of a stop codon at position 1498-1500. The resultant protein is truncated by 137 amino acids as compared to the SR-p70a protein (AAW36184). The sequence can be used in the diagnosis and monitoring of cancer, especially neuroblastoma. The nucleic acid sequences and corresponding antisense sequences, are also useful in gene therapy, e.g. to regulate apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -DIQIQANTLPKLENHNIGGYCFSMVLDE---PPKSL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 spytpehaasvpthspyagpsstfdtmspapvipsntdyp-gphhfevtfggsstaksat 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p73; splice variant; human; p73 beta; p53 tumour suppressor; E6; oncoprotein; inhibitor; apoptosis; human papilloma virus; HPV; cancer; uterine cervix; anogenital; oesophageal squamous cell; laryngeal papilloma; bronchiolo-alveolar; penile; bladder; carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 epdstyfdlpgssrgnnevvggtdssmdvfhlegmttsvmaqfnllsstmdgmssraasa 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQP-LNLRVFLCF--SNDVSAPVVRCQNHLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 LAFKFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58;
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larity 23.9%; Pred. No. 3.7e-11;
Conservative 47; Mismatches 143;
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 -RQLN--SKKRKSVPEAAEEDEPSKV 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 499 AA.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                               a splice
capable of
not targeted
                                                                                                                                                                                                                                   inhibitor of cancer colony growth and inducer of apoptosis. Apoptosis can be induced in E6-expressing cells, by administering p73 protein or DNA construct encoding p73. It can be used to treat human papilloma virus (HPV) infections, cancers of the uterine cervix, anogenital, oesophageal squamous cell cancer, laryngeal papilloma, and bronchiolo-alveolar, penile and bladder carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spytpehaasvpthspyaqpsstfdtmspapvipsntdyp-gphhfevtfqqsstaksat 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ilynfmcnsscvggmnrrpiliiitlemrdgqvlgrrsfegricacpgrdrkadedhyre 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -DIQIQANTLPKLENHNIGGYCFSMVLDE---PPKSL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQP-LNLRVFLCF--SNDVSAPVVRCQNHLS 161
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epdstyfdlpgssrgnnevvggtdssmdvfhlegmttsvmagfnllsstmdgmssraasa 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- 73
                                                                                                                                                                      The present sequence is a human p73 beta protein, which is a splice variant of p73. p73 is a homolog of p53 tumous suppressor, capable arresting the growth of E6 protein-expressing cells. It is not targ for degradation by E6 oncoprotein and has been found to be a potent
                                                                                            cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p53 promoter;
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                                                                                                                                                                                                                                                                                                                                                                                                                            58;
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                                                                                          using p73 to induce apoptosis in E6- expressing Human papillomavirus induced cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDDSTEVDIKEDIPKTVEVSGSELTTEPMAFLQGLNSGNLMQFSQQSVLREMMLQ-
                                                                                                                                                                                                                                                                                                                                                                                               Length 499;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p53 responsive element; inhibition.
                                                                                                                                                                                                                                                                                                                                                                                            9.5%; Score 191; DB 21;
larity 23.9%; Pred. No. 3.7e-11;
Conservative 47; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295
                                                                                                                                         45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -RQLN--SKKRKSVPEAAEEDEPSKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p73; antibody;
tumour; growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha protein.
                                                                                                                                         Claim 12; Page 42-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                               2000-136954/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW30661 standard;
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 78; Conser
                                                                                                                                                                                                                                                                                                                                                 499 AA;
                                                          N-PSDB; AAZ49690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; NBS-1;
p53-dependent
                                                                                            Novel methods
                                                                                                            to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                El-Deiry WS;
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                                                                                                                                                                                                                                                                                                                                                   Sequence
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A method has been developed for treating a subject having a p53-dependent tumour cell. The method comprises: (a) determining the level of NBS-1 protein (also known as p73) expressed in the tumour cell and in a corresponding non-malignant cell; (b) selecting subjects having NBS-1 protein level comparable or below that in a corresponding normal cell; (c) elevating tumour cell NBS-1 level, where NBS-1 interacts with p53-responsive promoters. Also described in the present invention is an antibody that specifically binds to NBS-1, and an antibody raised to the carboxy portion of NBS-1. NBS-1 can activate the transcription of p53-responsive genes and can inhibit cell growth in a p53-like manner. The present sequence represents the human NBS-1 alpha protein from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 wtyspllkklycqiak--tcpiqikvstppppgtairampvykkaehvtdvvkrcpnhel 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DIQIQANTLPKLENHNIGGYCFSMVLDE---PPKSL 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SR-p70; human; transcription factor; p53; tumour suppressor gene; homology; differential splicing; diagnosis; cancer; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 grdfneggsapashlirvegnnlsgyvddp----vtgrgsvvvpy----eppgvgteftt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 VEPLTANNAKMRESLLRSENPN-SVYCGNAQGKGISERFSVVVPLNMSRSVTRSGLTRQT
                                                                                                                                                                                                                                                                                                                                used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 EDDSTEVDIKEDIPKTVEVSGSELTTEPMAFLQGLNSGNLMQFSQQSVLREMMLQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 635;
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                                                                                                                                                                                                                                                                                                                           Treating subjects using NBS-1 proteins and antibodies interact with p53-responsive genes and inhibit growth of p53-dependent tumour cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human p53 tumour suppressor-related protein SR-p70a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.5%; Score 191; DB 20; llarity 23.9%; Pred. No. 5.4e-11; Conservative 47; Mismatches 143;
                                                                                   (DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 -RQLN--SKKRKSVPEAAEEDEPSKV 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Fig 1A; 65pp; English.
    97us-0046207
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                                                                                                                                                                                                                                               WPI; 1999-059690/05.
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                                                                                                                                                                  Kaelin W;
12-MAY-1997;
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<del>..</del>
07-APR-2000
                                                                                                  Homo sapiens
                                                                                                                        W09966946-A1
                                                                                                                                                                   23-JUN-1999;
                                                                                                                                                                                         24-JUN-1998;
                                                                                                                                                                                                                                      El-Deiry WS;
                                                                                                                                              29-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                       es related
                                                                                                                                                                                                                                                                             This is the amino acid sequence of the human protein SR-p70a. SR-p70 are transcription factors which may control the activity of p53-regulated genes, and are expressed by tumour suppressor genes relate to the p53 gene family. The gene sequence was isolated from the human colon adenocarcinoma cell line HT-29, using primers AAV01506-7. The sequence can be used in the diagnosis and monitoring of cancer, especially neuroblastoma. The nucleic acid sequences and corresponding antisense sequences, are also useful in gene therapy, e.g. to regulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220
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                                                                                                                                                                                                             New polypeptide(s) encoded by the SR-p70 tumour suppressor gene and related nucleic acid, useful for diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epdstyfdlpgssrgnnevvggtdssmdvfhlegmttsvmagfnllsstmdgmssraa
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -DIQIQANTLPKLENHNIGGYCFSMVLDE-
                                                                                                                                                                                                                                                                                                                                                                                                                           9.5%; Score 191; DB 18;
larity 23.9%; Pred. No. 5.5e-11;
Conservative 47; Mismatches 143;
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                                                                                                                                                        Kaghad
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                                                                                      97WO-FR00214
                                                                                                           96FR-0001309
 apoptosis
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N-PSDB; AAV01498.
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                                                                                                                                                                                                                                                                                                                                                                                             636 AA;
                                                                                                                                                        Ferrara
                                                                                                                                                                                                                                                          Claim 7; Fig 6;
                                                                                                                                 (SNFI ) SANOFI
gene therapy;
                      Homo sapiens
                                          WO9728186-A1
                                                                                     03-FEB-1997;
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                                                                                                            02-FEB-1996;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 spytpehaasvpthspyaqpsstfdtmspapvipsntdyp-gphhfevtfqqsstaksat 141
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                                                                                                                                             p73; splice variant; human; p73 alpha; p53 tumour suppressor; E6; oncoprotein; inhibitor; apoptosis; human papilloma virus; HPV; cancer; uterine cervix; anogenital; oesophageal squamous cell; laryngeal papilloma; bronchiolo-alveolar; penile; bladder; carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a human p73 alpha protein, which is a splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressing cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel methods using p73 to induce apoptosis in E6-used to treat Human papillomavirus induced cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143;
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                                                                       Human p73 alpha splice variant protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Page 40-41; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -RQLN--SKKRKSVPEAAEEDEPSKV 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ49690
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7

AAW36183;

Monkey

AAW36183

AAW36183

RESULT

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cells. SR-p70 are transcription factors which may control the activity of p53-regulated genes, and are expressed by tumour suppressor genes related to the p53 gene family. The gene sequence was isolated from a cDNA library by sequencing the inserts and comparing to sequence databases. The protein sequence contains regions of homology to the p53 protein. A second sequence (SR-p70b) was also isolated from the library and was caused by differential splicing of the sequence (see AAV01497). The sequences can be used in the diagnosis and monitoring of cancer, especially neuroblastoma. The nucleic acid sequences and corresponding antisense sequences, are also useful in gene therapy, e.g. to regulate
                       -DIQIQANTLPKLENHNIGGYCFSMVLDE---PPKSL 104
                                                                                                                                                                                                                                                                                                                                                                             SR-p70; monkey; transcription factor; p53; tumour suppressor gene; homology; differential splicing; diagnosis; cancer; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the amino acid sequence of the protein SR-p70a from monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 epdstyfdlpgssrgnnevvggtdssmdvfhlegmttsvmaqfnllsstmdgmssraasa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SR-p70 tumour suppressor gene
for diagnosis and treatment of
LAFKFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 EDDSTEVDIKEDIPKTVEVSGSELTTEPMAFLQGLNSGNLMQFSQQSVLREMMLQ-
                                                                                                                                                                                                                                                                                                                                       Monkey p53 tumour suppressor-related protein SR-p70a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ed. No. 7e-1
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide(s) encoded by the SR-and related nucleic acid, useful for
                                                                               295
                                                                                                                 312 qqalnessakngaaskrafkqsppav 337
                                                                                                                                                                                                                    AAW36182 standard; Protein; 637 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaghad AM;
                                                                            -RQLN--SKKRKSVPEAAEEDEPSKV
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                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecus aethiops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ferrara P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV01496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SNFI ) SANOFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apoptosis.
                                                                                                                                                                                                                                                           AAW36182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caput D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18
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                                                                                                                                                                                                                                                                                                                                                                            SR-p70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumours
                                                                                                                                                                               ]]
                                      252
 221
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PF
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  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               databases. The protein sequence contains regions of homology to the p53 protein. The SR-p70b gene sequence was isolated simultaneously with the SR-p70a sequence (AAV01496) from the library and is created by differential splicing of the SR-p70 mRNA sequence. The sequences can be used in the diagnosis and monitoring of cancer, especially neuroblastoma. The nucleic acid sequences and corresponding antisense sequences, are also useful in gene therapy, e.g. to regulate apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes
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                                                                                                                                                                                                ene;
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                                                                                                                                                                                                                    oma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQP-LNLRVFLCF--SNDVSAPVVRCQNHLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEPLTANNAKMRESLLRSENPN-SVYCGNAQGKGISERFSVVVPLNMSRSVTRSGLTRQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the amino acid sequence of the protein SR-p70b from monk cells. SR-p70 are transcription factors which may control the acof p53-regulated genes, and are expressed by tumour suppressor grelated to the p53 gene family. The gene sequence was isolated cDNA library by sequencing the inserts and comparing to sequence databases. The protein sequence contains regions of homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SR-p70 tumour suppressor gene for diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58;
                                                                                                                                                                                             suppressor g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wtyspllkklycqiak--tcpiqikvsappppgtairampvykkaehvtdivkrcpn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 EDDSTEVDIKEDIPKTVEVSGSELTTEPMAFLQGLNSGNLMQFSQQSVLREMMLQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    499;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                     p53 tumour suppressor-related protein SR-p70b.
                                                                                                                                                                                           SR-p70; monkey; transcription factor; p53; tumour su
homology; differential splicing; diagnosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 18;
.7e-11;
es 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 190; DB 18
Pred. No. 4.7e-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                   standard; Protein; 499 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaghad AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 5; 136pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.58;
                                                                                                                                                                                                                                                                                                                                                                                          97WO-FR00214
                                                                                                                                                                                                                                                                                                                                                                                                                                  96FR-0001309
                                                                                                               entry)
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                                                                                                                                                                                                                                   gene therapy; apoptosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ferrara P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide(s) eand related nucleic
                                                                                                               (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV01497
                                                                                                                                                                                                                                                                         Cercopithecus
                                                                                                                                                                                                                                                                                                               WO9728186-A1
                                                                                                                                                                                                                                                                                                                                                                                         03-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                  02-FEB-1996;
                                                                                                             27-APR-1998
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Sequence

Query Match

Matches

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105

Qγ

83

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142

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162

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200

Gaps

Indels

Length 637;

71

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spytpehaasvpthspyaqpsstfdtmspapvipsntdyp-gphhfevtfqqsstaksat 141

83

105

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200

Db

273

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312

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15;

80;

Indels

124;

Length 448;

DB 20;

-wpqytnlg 76

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89 GGYCFSMVLDE---PPKSLWMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF 145
                                                                                                                                                                                                                                                                        --SNDVSAPVVRCQNHLSVEPLTANNAKMRESLLRSENPNSVYCGNAQGKGISE----RF 199
                                                                                                                                                                                                                                                                                                       193 kkaehvtevvkrcpnhelsrefneggiappshlirve----gnshagyvedpitgrg 245
                                                                                                                                                                                                                                                                                                                                                          246 svlvpy----eppgvgtefttvlynfmcnsscvggmnrrpiliivtletrdggvlgrrcf 301
                                                                   QPMSWHKESTDSEDDST-EVDIKEDIPKTVEVSGSELTTEPMAFLQGLNSGNLMQFSQQS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the intron-exon organisation is conserved between p73 and p53, and from
                                                                                                                                                       200 SVVVPLNMSRSVTRSGLTRQTLAFKFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell regulatory protein; p63; huTAp63 gamma; TAp63 gamma; human; cancer; tumour suppressor; cell cycle control; apoptosis; cell proliferation; cell differentiation; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated p63 cell regulatory protein for, e.g. treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cell regulatory protein p63, isoform huTAp63 gamma.
                                                                                        257 HVKICTCPKRDRIQDERQLNSKKRKSVPEAAEEDEPSK 294
                                                                                                                                                                                                                                                                                                                                                                                                                             :|| || || || || 302 earicacpgrdrkade---dsirkqqvsdstkngdgtk 336
    Score 186; DB 2
Pred. No. 1e-10;
                      ed. No. le-1
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY05955 standard; Protein; 448 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 23; Fig 11; 161pp; English.
                                                                                                                                     64 VLREMMLQDIQIQ---ANTLPKLENH-
                                 59;
    9.3%;
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97US-0062076.
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                                    Conservative
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)B; AAX58574.
                  Similarity 75; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens,
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15-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY05955;
  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a human p51 protein, which is related tp53 and has cell proliferation regulation and tumour suppression activity. The p51 gene can be used in the investigation, diagnosis and treatment of diseases such as cancer, with which the p53 family cell proliferation regulation is associated. The p51 protein may be used for screening potential agonists and antagonists of its regulatory function for use as drugs,
                                                                                                                                  272
                  220
                                                                                                   251
LS 161
                                                                                                                                                                     re 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer;
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                                                             VEPLTANNAKMRESLLRSENPN-SVYCGNAQGKGISERFSVVVPLNMSRSVTRSGLTRQT
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proliferat
-SNDVSAPVVRCQNHI
                                                                                                                                                  cell proliferation; regulation;
                                                                                                                                LAFKFVCQNSCIG - - - RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for diagnosis, potential cell
                                                                                 WMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQP-LNLRVFLCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142..321
/label= DNA_binding_domain
353..397
/label= oligomerisation_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transactivation_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 147-148; 163pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene p51, useful and screening for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    448 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; p51; p53 related gene;
tumour suppression; diagnosis
                                                                                                                                                                                                                                                                                                                   AAY45246 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98JP-0100467
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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/label=
142..321
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                                                                                                                                                                                                                                                                                                                                                                                                                     Human p51 protein
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Homo sapiens

Domain

Domain

Domain

07-JAN-2000

XX

448 AA;

Sequence

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treatment

New p53

24-MAR-1999;

07-OCT-1999

27-MAR-1998;

Ikawa Y,

N-PSDB;

WO9950412-A1

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known exon and intron sizes for these 2 genes, it was possible to identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosomal position 3427-29. At least 6 different isotypes exist. Splice variants differing at the C-terminus have been designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are designated as deltan and TA forms, where the deltan form lacks the transactivation domain. The present sequence represents human p63 isotype TAp63 gamma. p63 was detected in a veriety of thuman and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or fown-regulation of p63 expression may play a critical role in the process of cervical squamous differentiation, both benign and necelastic Deltan isotopes of p63 act as dominant negatives towards transactivation by p53 and p63. p63 may also be implicated in haematopoiesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AAX0593-64), polynucleotides (see AAX58972-83) and anti-p63 antibodies of the invention can be used to identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of transgenic animals.
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                                                                                                                                                                                                                          expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --PPKSLWMYSIPLNKLYIRMNKAFNVDV.)FKSKMPIQPLNLRVFLCF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                         of p63
                                                                                                                                                                                                                                                                                                                                     (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                     used to
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This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit
                                                                                                                                                                                                                                                                                                                                                       cancer
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30-DEC-1999;
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The present invention concerns the discovery of a new family of cell regulatory proteins (CRRs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tunnour suppressor proteins p53 and p73. It has been observed that the intron-exon and intron sizes for these 2 genes, it was possible to intron-exon and intron sizes for these 2 genes, it was possible to identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosomal position 3427-29. At least 6 different isotypes exist. Splice variants of intron. The human p53 members differing in the N-terminus are designated as deltan and members differing in the N-terminus are designated as deltan and new forms, while p63 members differing in the N-terminus are designated as deltan and nowns, where the deltan form lacks the transactivation domain. The present sequence represents human p63 isotype a TAP63 beta. p63 was detected in a variety of activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous differentiation, both benign and neoplastic. Deltan isotopes of p63 may also be implicated in haematopolesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative of disorders. p63 polypeptides (see AAV56553-64), polynucleotides (see AAX58572-83) and anti-p63 antibodies of the invention can be used to processes, in detection and diagnosis, and in the production of transcent and in derection and diagnosis, and in the processes. e.g. treatment of Cell regulatory protein; p63; huTAp63 beta; TAp63 beta; human; cancer; tumour suppressor; cell cycle control; apoptosis; cell proliferation; cell differentiation; then py. regulatory protein p63, isoform huTAp63 beta New isolated p63 cell regulatory protein for, Claim 23; Fig 10; 161pp; English. 98US-0087216. 97US-0062076. 98WO-US21992 (HARD) HARVARD COLLEGE WPI; 1999-277595/23 N-PSDB; AAX58573. transgenic animals. Yang A; 516 AA; Homo sapiens. WO9919357-A2. 29-MAY-1998; 15-OCT-1997; 22-APR-1999. 02-OCT-1998; 16-AUG-1999 cell McKeon F, Seguence tumours WPI

59; Conservative

Gaps NI 88 QPMSWHKESTDSEDDST-EVDIKEDIPKTVEVSGSELTTEPMAFLQGLNSGNLMQFSQQS 63 --wpqytnlg 76 80; Length 516; Indels 124; ||: : |||:|:::|| | :::|| qpidlnfvdepsedgatnkieismd---cirmgdsdl-sdpm-9.3%; Score 186; DB 20; 22.2%; Pred. No. 1.3e-10; ed. No. 1.3e Mismatches VLREMMLQDIQIQ -- -ANTLPKLENH -Query Match Best Local Similarity 64 ń

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77 llnsm---dqqiqngssstspyntdhaqnsvtapspyaqpsstfdalspspaipsntdyp 133 89 GGYCFSMVLDE---PPKSLWMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF 145 --SNDVSAPVVRCQNHLSVEPLTANNAKMRESLLRSENPNSVYCGNAQGKGISE----RF 199 200 SVVVPLNMSRSVTRSGLTRQTLAFKFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVI 256 246 svlvpy----eppqvgtefttvlynfmcnsscvggmnrrpiliivtletrdgqvlgrrcf 301 257 HVKICTCPKRDRIQDERQLNSKKRKSVPEAAEEDEPSK 294 146 d g QY Q g QΫ Qγ

Search completed: November 16, 2001, 15:49:07 Job time: 2734 sec

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8, A 9, A 12,

Sequence Sequence

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2, A 32,

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32, Appl 9, Appli 2, Appli

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105 WMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF--SNDVSAPVVRCQNHLSV 162
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Pred. No. 2.4e-11;
; Mismatches 109;
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US-08-801-718-8
US-08-801-718-9
US-08-247-904B-12
US-08-675-631-1
US-08-392-542-2
US-08-392-542-2
US-08-328-673A-9
US-08-328-673A-9
US-08-894-327-2
PCT-US95-15353-2
US-08-697-221-15
US-08-697-221-17
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                                                                                                                                                                                                                   Tumour Suppressor Gene
                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                 US/09/257,580
                                                                                                                                                                                                           Yorkshire Cancer Research
                                                                                                                                                                                                               TITLE OF INVENTION: Tumour Suppressor FILE REFERENCE: Canine p53 CURRENT APPLICATION NUMBER: US/09/257 CURRENT FILING DATE: 1999-02-25 PRIOR PPLICATION NUMBER: 9804178.3 PRIOR FILING DATE: 1998-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-347-792-15; Sequence 15, Application US/08347792; Patent No. 5573925
                                                                                                                                                                                    Sequence 2, Application US/09257580 Patent No. 6307036
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GENERAL INFORMATION:
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CLASSIFICATION:
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US-08-431-357-15
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25.6%; Pred. No. 1.3e-09;
ive 38; Mismatches 95;
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GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos D.
TITLE OF INVENTION: p53 Proteins With Altered
TITLE OF INVENTION: Tetramerization Domains
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: p53 Proteins With AlteralITLE OF INVENTION: Tetramerization Domains NUMBER OF SEQUENCES: 37
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SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0,
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Spring House
Pennsylvania
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Patent No. 5721340
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
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NAME: Bak, Mary E.
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FILING DATE:
CLASSIFICATION: 530
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OPERATING SYSTEM:
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US-08-431-357-15
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VENTION: Peptides nad Peptidomimetics with
VENTION: Structural Similarity to Human p53 That Activate p53
VENTION: Function
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
MPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Pred. No. 1.3e-09;
8; Mismatches 95;
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                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/347,792
FILING DATE: 28-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
                                                                                                                                                                                                                                                                                                                                        WST58USA
                                                                                                                                       US/08/431,357
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APPLICANT: Halazonetis, Thanos
APPLICANT: Hartwig, Wolfgang
TITLE OF INVENTION: Peptides nad
TITLE OF INVENTION: Structural Signature.
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District of Columbia
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                                                                                                                                                                                                                                                                                        NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
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TELEFAX: 215-540-5818
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                                                                                                             CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                                                                                                                                    APPLICATION NUMBER:
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Best Local Similarity
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                                YSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF -- SNDVSAPVVRCQNHLSVEP 164
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                                                                                                                                                                                                                                                    278 KKRKSVPEAAEEDEPSKVRRCIAIKTEDTESNDSRDCDDSAAEWNVSRTPDGDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spring House Corporate Cntr., PO Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.3%; Score 167.5; DB 5; 25.6%; Pred. No. 1.3e-09; Wiematches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: The Wistar Institute of Anatomy APPLICANT: and Biology APPLICANT: Halazonetis, Thanos D. TITLE OF INVENTION: p53 Proteins With Altered TITLE OF INVENTION: Tetramerization Domains
                                                                                                     LTANNAKMRESLLRSENPNSVYCGNAQGKGISE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT/US95/15353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WST58CPCT
                                                                                                                                                                                                                                                                                        288 KKEVLCPEL----PPGSAKRALPTCT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/456,623
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 08/347,792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/431,357 FILING DATE: 28-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application PC/TUS9515353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31,215
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TELEPHONE: 215-540-9206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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REFERENCE/DOCKET NUMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spring House
Pennsylvania
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Best Local Similarity
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PCT-US95-15353-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 YSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF--SNDVSAPVVRCQNHLSVEP 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Sequence 3, Application US/08894327

GENERAL INFORMATION:

APPLICANT: Halazonetis, Thanos

APPLICANT: Hartwig, Wolfgang

TITLE OF INVENTION: Peptides and peptidomimetics with

TITLE OF INVENTION: Structural similarity to human p53 that activate

TITLE OF INVENTION: function

FILE REFERENCE: 2973.19998

CURRENT FILING DATE: 1997-12-04

EARLIER APPLICATION NUMBER: pctus96/01535

EARLIER APPLICATION NUMBER: 08/392,542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 LAFKFVCQNSCIG -- - RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQLNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 LTANNAKMRESLLRSENPNSVYCGNAQGKGISE----RFSVVVPLNMSRSVTRSGLTRQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 IHYKYMCNSSCMGGMNRRPILTITLEDSSGNLLGRDSFEVRVCACPGRDRRTEEENFR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 YSPPLNKLFCQLVKTCPVQL-WVSATPPAGSRVRAMAIYKKSQHM1EVVRRCPHHER(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 390;
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Pred. No. 1.3e-∪9;
38; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                8.3%; Score 167.5; DB 4;
ilarity 25.6%; Pred. No. 1.3e-09;
Conservative 38; Mismatches 95;
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                                                                                                                                       0486.48439
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EARLIER FILING DATE: 1995-02-16
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version
288 KKEVLCPEL----PPGSAKRALPTCT
                                                                                                                       34,698
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                                                                                                                                     REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9299
TELEFAX: 202 508-9299
                                                                                                                                                                             TELEFAX: 202 300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                      Laurence
                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence
REGISTRATION NUMBER: 34,
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                                                                                                                                                                                                                                                                                        unknown
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                                                                                                                                                                                                                                                                                                                        ) MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Mus spretus
US-08-392-542-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 514
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; ORGANISM: Mus spretus
US-08-894-327-3
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Best Local Similarity
Matches 60; Conser
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TOPOLOGY: lir
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US-08-894-327-3
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                 CURRENT
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           EP 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 YSPALNKMFCQLAKTCPVQLWVDSTPP-PGTRVRAMAIYKQSQHMTEVVRRCPHHERCS- 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF -- SNDVSAPVVRCQNHLSVEP 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                LAFKFVCQNSCIG --- RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQLNS
                                                                                                                                               LTANNAKMRESLLRSENPNSVYCGNAQGKGISE----RFSVVVPLNMSRSVTRSGLTRQT
                                                                                                 ---GNLYPEYLEDROTFRHSVVVPY----EPPEAGSEYTT
                                     YSPPLNKLFCQLVKTCPVQL-WVSATPPAGSRVRAMAIYKKSQHMTEVVRRCPHHERC
                                                                                                                                                                                             331
         YSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF -- SNDVSAPVVRCQNHLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                          KKRKSVPEAAEEDEPSKVRRCIAIKTEDTESNDSRDCDDSAABNNSRTPDGDY
                                                                                                                                                                                                             --SASPPOKKRPLDGEY
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Pred. No. 5.3e-09;
                                                                                                                                                                                                                                                                                                                                                             Constructs
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PQ
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:: WST64AUSA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,802
FILING DATE: 22-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/697,22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Floppy disk
IBM PC compatible
YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Halazonetis, Thanos D. TITLE OF INVENTION: Modified p53 TITLE OF INVENTION: Therefor
                                                                                                                                                                                                                                                                                                3, Application US/08697221
). 5847083
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23.0%; Pre
52;
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Spring House Corpora
                                                                                                                                                                                                                      288 KKEVLCPEL----PPGSAKRALPTCT
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amino acid
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                                                                                     215-540-5818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                Patent No. 5847083
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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INFORMATION FOR
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                                                                                                                                                                                                                                                                                   US-08-697-221-3
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CITY: S
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 YSPALNKMFCQLAKTCPVQLWVDSTPP-PGTRVRAMAIYKQSQHMTEVVRRCPHHERCS- 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                             278 KKRKSVPEAAEEDEPSKVRRCIAIKTEDTESNDSRDCDDSAAEWNVSRTPDGDY-RLAIT
                                   LAFKFVCQNSCIG - - - RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQLNS
                                                        232 IHYNYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGRDRRREEENLRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 LTANNAKMRESLLRSENPNSVYCGNAQGKGISE----RFSVVVPLNMSRSVTRSGLTRQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - EPPEVGSDCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44;
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Halazonetis, Thanos D.
TITLE OF INVENTION: Modified p53 Constructs and Uses
TITLE OF INVENTION: Therefor
                                                                                                                                                                                         337 CPNKEWLLQSIEGMIKEAAAEVLRNPNQENLRRHANKLLSLK 378
                                                                                                                                                                                                                   GRERFEMFRELNEALELKDAQAGKEPG--GSRAHSSHLKSKK 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DSDGLAPPQHLIRVE-----GNLRVEYLDDRNTFRHSVVVPY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ittentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spring House Corporate Cntr., PO Box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 162; DB 2;
Pred. No. 5.3e-09
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(IOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/697,221
                                                                                                                                                    292 K----GEPHHELPPGSTKRALPNNT----
                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08697221 Patent No. 5847083 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33,980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.18; 23.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cathy A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acid
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 -DSDGLAPPQHLIRVE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UZIP: 19477
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US-08-047-041A-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS:
                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                             APPLICANT:
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PAGES:
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STATE:
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                                          KKRKSVPEAAEEDEPSKVRRCIAIKTEDTESNDSRDCDDSAAEWNVSRTPDGDY-RLAIT 336
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-SSSPQPKKKPLDGEYFTLQIR 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 YSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF--SNDVSAPVVRCQNHLSVEP 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 LTANNAKMRESLLRSENPNSVYCGNAQGKGISE----RFSVVVPLNMSRSVTRSGLTRQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSPALNKMFCQLAKTCPVQLWVDSTPP-PGTRVRAMAIYKQSQHMTEVVRRCPHHER(
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                                                                                                                                                                                                                                                                      and Uses
                                                                                                                       106;
                                                                                                                                                                                                                                                                                                                                             PO Box
                                                                                                    337 CPNKEWLLQSIEGMIKEAAAEVLRNPNQENLRRHANKLLSLK
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Pred. No. 7.7e-09;
17; Mismatches 106
                                                                                                                                                                                                                                                                     Constructs
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           Spring House Corporate Cntr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DALE.

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,802
FILING DATE: 22-SEP-1995
ATTORNEY/AGENT INFORMATION:
...MD. Kodroff, Cathy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WST64AUSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/697,221
                                                                                                                                                                                                                                                   APPLICANT: Halazonetis, Thanos D. TITLE OF INVENTION: Modified p53 TITLE OF INVENTION: Therefor
                                                                                                                                                                                                         Sequence 18, Application US/08697221
Patent No. 5847083
                                                                        --GEPHHELPPGSTKRALPNNT--
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TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
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amino acid
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                       Spring House
Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                       Patent No. 5847083
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                      USA
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CITY: S
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Best Local
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278 KKRKSVPEAAEEDEPSKVRRCIAIKTEDTESNDSRDCDDSAAEWNVSRTPDGDYRLAITC 337
                                   ---SSSPQPKKKPLDGEY---
                                                                                                                                                                                                                                                                                                                      Detection of Loss of the Wild-Type p53
                                                                   338 PNKEWLLQSIEGMIKEAAAEVLRNPNQENLRRHANKLLSLK 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version #1.25
                                                                                          INGRERFEMFRELNEALELK
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STREET: 1001 G Street, N.W.
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FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 07/928,661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                             Sequence 25, Application US/08047041A Patent No. 5527676
                                K----GEPHHELPPGSTKRALPNNT
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TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
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                                                                                                                                                                                                                                                                    Baker, Suzanne J
                                                                                                                                                                                                                                                   Vogelstein, Bert
                                                                                                                                                                                                                                                                                 APPLICANT: Fearon, Eric R.
APPLICANT: Nigro, Janice M.
TITLE OF INVENTION: Detecti
TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0'
FILING DATE: 06-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 17-AUG-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393 amino acids
amino acid
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APPLICATION NUMBER: US
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YES
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APPLICATION NUMBER:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                              Patent No. 5527676
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-5(INFORMATION FOR SEQ
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                      Gaps
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                                                                                                                                               --EPPEVGSDCTT
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                                               107 YSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF--SNDVSAPVVRCQNHLSV
                                                                             YSPALNKMFCQLAKTCPVQLWVDSTPP-PGTRVRAMAIYKQSQHMTEVVRRCPHHERC
                                                                                                             165 LTANNAKMRESLLRSENPNSVYCGNAQGKGISE----RFSVVVPLNMSRSVTRSGLTR
                    44;
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Fearon, Eric R.
Nigro, Janice M.
VENTION: Detection of Loss of the Wild-Type p53
                    Indels
                                                                                                                                           -DSDGLAPPQHLIRVE-----GNLRVEYLDDRNTFRHSVVVPY--
                                                                                                                                                                                                                                                                                                      CPNKEWLLQSIEGMIKEAAAEVLRNPNQENLRRHANKLLSLK 378
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ZIP: 20001.4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 8.8e-09;
ches 122;
                                                                                                                                                                                                                                                                                                                           Pred. No. 8.86; Mismatches
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22-MAR-1993
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ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/446,584 FILING DATE: 06-DEC-1989 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/08047041A Patent No. 5527676
                                                                                                                                                                                                                                                                      --GEPHHELPPGSTKRALPNNT-
  ilarity 23.0%; Pr
Conservative 51;
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Raker, Suzanne J
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REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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l Similarity
65; Conserv
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APPLICANT:
APPLICANT:
    Best Local
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--SSSPQPKKKPLDGEYFTLOIR 333
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Nigro, Janice M.
VENTION: Detection of Loss of the Wild-Type p53
                                                                                                                                                                                                                                                                   Length 393;
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23.0%; Pred. No. 8.8e-09;
ive 51; Mismatches 122;
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FILING DATE: 17-AUG-1992
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Patent No. 5527676
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
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STREET: 1001 G Street, N.W.
CITY: Washington
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Baker, Suzanne J
                                                                                                     Harris, et al.,
Mol. Cell. Biol
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                                                                 ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                Conservative
  protein
YES
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                                                                                                                                                                        4650-4656
1986
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                ORIGINAL SOURCE:
MOLECULE TYPE:
                                                                                                                                                                                       ; DATE: 1980
US-08-047-041A-26
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APPLICANT:
                                 ANTI-SENSE:
                                                                                                                                                                                                                                                                                              65;
                                                                                                 AUTHORS:
                                                                                                                        JOURNAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the Wild-Type p53
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larity 23.0%; Pred. No. 8.8e-09;
Conservative 51; Mismatches 122
                                                                                        32,141
R: 01107.42917
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                           MBER: US 07/330,566
29-MAR-1989
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GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Baker, Suzanne J.
APPLICANT: Fearon, Eric R.
APPLICANT: Nigro, Janice M.
TITLE OF INVENTION: Detection of
                                                                        NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
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                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Harris, et al.,
JOURNAL: Mol. Cell. Biol
06-DEC-1989
                                                                                                                                                                                                 393 amino acids
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                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
              PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner &
                           APPLICATION NUMBER:
FILING DATE: 29-MA
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4650-4656
1986
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US-08-047-041A-28
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-08-047-041A-27
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Best Local S
Matches 65
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126 YSPALNKMFCQLAKTCPVQLWVDSTPP-PGTRVRAMAIYKQSQHMTEVVRRCPHHERCS- 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---SSSPQPKKKPLDGEYFTLQIR 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 LAFKFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQLNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 LTANNAKMRESLLRSENPNSVYCGNAQGKGISE----RFSVVVPLNMSRSVTRSGLTRQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278 KKRKSVPEAAEEDEPSKVRRCIAIKTEDTESNDSRDCDDSAAEWNVSRTPDGDY-RLAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44;
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                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 160; DB 1;
Pred. No. 8.8e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                              01107.42917
                                                                                                                                   US/08/047,041A
                                                                                                                                                                                                                                                                                                                 MBER: US 07/330,566
29-MAR-1989
                                                                                                                                                                                                        us 07/928,661
                                                                                                                                                                                                                                                               MBER: US 07/446,584
06-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GEPHHELPPGSTKRALPNNT---
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23.08; Pre
                                                                                                                                                                                                                                                                                                                                                                                             32,141
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
ZIP: 20001.4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                  22-MAR-1993
                                                                                                                                                                                                                      17-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 amino acids
                                                                                                               CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                            Sarah A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lamb, P.
Crawford, L.
                                                                                                                                                                                                      APPLICATION NUMBER:
FILING DATE: 17-AUG-PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                              FILING DATE: 06-DEC-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                             NAME: Kagan, Sarah REGISTRATION NUMBER:
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1986
                                                                            OPERATING SYSTEM:
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                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                   FILING DATE:
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                                                                                                SOFTWARE:
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                                                            COMPUTER;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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OPERATING
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   APPLICANT:
APPLICANT:
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                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --SSSPQPKKKPLDGEYFTLQIR 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                  PO Box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 GRERFEMFRELNEALELKDAQAGKEPG--GSRAHSSHLKSKK
                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 160; DB 1;
Pred. No. 8.8e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 LTANNAKMRESLLRSENPNSVYCGNAQGKGISE----RFSV
                                                                                         Altered
                                                                        APPLICANT: Halazonetis, Thanos D. TITLE OF INVENTION: p53 Proteins With AlteralILE OF INVENTION: Tetramerization Domains NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                 Spring House Corporate Cutr.,
                                                                                                                                                                                                                                                                                                                                                                                                                         WST58USA
                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5708136
GENERAL INFORMATION:
APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---GEPHHELPPGSTKRALPNNT--
                            2, Application US/08347792
0, 5573925
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                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WS'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.0%;
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                     NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                             Spring House
Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                             Bak, Mary E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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nes 65; Conser
                                          Patent No. 5573925
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
US-08-347-792-2
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                                                                                                                                                                                                           COUNTRY: US
ZIP: 19477
                                                                                                                                                   ADDRESSEE:
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             US-08-347-792-2
                                                                                                                                                                 STREET:
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                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 YSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF -- SNDVSAPVVRCQNHLSVEP 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAFKFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQLNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -DSDGLAPPQHLIRVE-----GNLRVEYLDDRNTFRHSVVVPY----EPPEVGSDCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 LTANNAKMRESLLRSENPNSVYCGNAQGKGISE----RFSVVVPLNMSRSVTRSGLTRQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 393;
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                                AMPLIFICATION OF HUMAN MDM2 GENE IN HUMAN TUMORS
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                                                                                                                                                                                                                                                                                                   Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 160; DB 1; I
Pred. No. 8.8e-09;
1: Mismatches 122;
                                                                                                            E: BANNER, BIRCH, MCKIE AND BECKETT 1001 G STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01107.42798
                                                                                                                                                                                                                                                                                                                                      US/08/390,516C
                                                                                                                                                                                                                                                            IBM PC compatible
XYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K----GEPHHELPPGSTKRALPNNT
KENNETH W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    32,141
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TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
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                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 07-APR-1993 CLASSIFICATION: 530
                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                               NAME: KAGAN, SARAH A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBLICATION INFORMATION:
AUTHORS: Buchman, et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                VOGELSTEIN,
                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                       NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
 KINZLER,
                                 TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                 WASHINGTON
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11;

Search completed: November 16, 2001, 15:49:51 Job time: 2648 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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- protein search, using sw model OM protein

Seconds ; Search time 46.24 Se (without alignments) 634.239 Million cell November 16, 2001, 15:10:08 Run on:

pdates/sec

US-09-524-101-2 2008 Title: Perfect score:

1 MYISQPMSWHKESTDSEDDS..........NLRRHANKLLSLKKRAYELP 385 Sequence:

BLOSUM62 Gapop 10.0 , Gapext Scoring table:

0.5

219241 hits satisfying chosen parameters: Total number of

219241 seqs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database

1; pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Cellular tumor ant	ellular	ellular tumor	llular tumor	llular tumor	llular tumor	lular	nor suppresso	Suppressor	lar tumor	llular tumor an	ar tumor an	beta-qalactosidase	vitellogenin II pr		hypothetical profe		-	ď	othetical		het	netical	cal	netical	fic seri	ntiden	box-binding pr	ypothetical pr
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		,((3)	ĸ	4	2	9	7	∞ ·																				28	

9

Gaps

22;

9.1%; Score 183; DB 1; Length 391; 27.0%; Pred. No. 2.3e-07; ive 36; Mismatches 99; Indels

Conservative

Similarity

Query Match Best Local S Best Loc Matches 107 YSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF--SNDVSAPVVRCQNHLSVEP 164

g

Dp

Qγ

165 LTANNAKMRESLLRSE-NPNSVYCGNAQGKGISERFSVVVPLNMSRSVTRSGLTRQTLAF 223

224 KFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQLNSKKR 280

233 KYMCNSSCMGGMNRRPILTITLEDSSGNLLGRDSFEVRVCACPGRDRRTEEENFR-KKE 291

qq

δ

QY

q

281 KSVPEAAEEDEPSKVRRCIAIKTEDTESNDSRDCD 315

: || : | : | : | 292 EHCPEL----PPGSAKRALPTSTSSSPQQKKKPLD 322

calcium-dependent	hypothetical prote	2	٠		4	intion fa	hypothetical prote	hypothetical prote	٠, -	hypothetical prote		- 0	probable disease r	multimeria podoth	_
184505	S51435	140487	T27053	T20968	C96829	T46637	C71607	T47961	T32650	B71717	T52425	E69026	T05250	A57384	0537
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ALIGNMENTS

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nucleus; pho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cellular tumor antigen p53 - golden hamster
N;Alternate names: tumor-suppressor protein p53
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JH0633
R;Legros, X.; McIntyre, P.; Soussi, T.
Gene 112, 247-250, 1992
A;Title: The cDNA cloning and immunological characterization of hamster p53.
A;Reference number: JH0633; MUID: 92210007
A;Reference number: JH0633
A;Molecule type: mRNA
A;References: GB:M75144; NID: g191414; PIDN: AAA37085.1; PID: g191415
A;Experimental source: Kidney, strain MP1
C;Genetics:
A;Gene p53
C;Genetics:
A;Gene: p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus F;179,182,241,245/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                             *status predicted
                                        A; Molecule type: mRNA
A; Residues: 1-51, 'S', 53-70, 72-293, 295-363 < HOW>
A; Residues: 1-51, 'S', 53-70, 72-293, 295-363 < HOW>
A; Cross-references: EMBL: X77546; NID: 9468513; PIDN: CAA54672.1; PID: 9468514
C; Genetics:
A; Gene: p53
C; Superfamily: cellular tumor antigen p53
C; Superfamily: cellular tumor antigen p53
C; Superfamily: cellular tumor antigen p53
C; Keywords: apoptosis; cell division control; DNA binding; homotetramer; nu F; 150, 153, 213, 217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F; 362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 CTYSPELNKLFCQLAKTCPLLVRVESPPPRGSI-LRATAVYKKSEHVAEVVKRCPHHERS 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 YSIPLNKLYIRMNKAFNVDVQFKSKMP----IQPLNLRVFLCFSNDVSAPVVRCQNHLSV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 YSPSINKLFCQLAKTCPVQLWVSSTPPPGTRVRAMAIYKKLQYMTEV---VRRCPHH--E 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPLTANNAKMRESLLRSE-NPNSVYCGNAQGKGISERFSVVVPLNMSRSVTRSGLTRQTL 221
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 VEPLTANNAKMRESLLRSENPNSVYCGNAQGKGI----SERFSVVVPLNMSRSVTRSGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 RQTLAFKFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQ
                                                                                                                                                                                                                                                                                                                                                                         41;
                                                                                                                                                                                                                                                                                                                             Length 363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 NYTKKRGLKPSGKRELAHPPSSEPPLPKKRLVVVDDDEE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 LNSKKRKSVPEAAEE-----DEPSKVRRCIAIKTEDTE 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.7%; Score 174; DB 1;
24.9%; Pred. No. 1.3e-06;
tive 51; Mismatches 118
                                                                                                                                                                                                                                                                                                                        Score 176.5; DE Pred. No. 7e-07;
                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   55 NLMQFSQQSVLREMMLQDIQIQANTLPKLENHNI---
                                                                                                                                                                                                                                                                                                                                                                        46;
                                                                                                                                                                                                                                                                                                                        8.8%;
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A; Reference number: A; Accession: S72313
                                                                                                                                                                                                                                                                                                                                                                    73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cellular tumor antigen p53 - African clawed frog c. Species: Xenopus laevis (African clawed frog) C. Species: Xenopus laevis (African clawed frog) C. Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-199 C; Accession: A29376; S61531; S72313; IS1639 R; Soussi, T.; de Fromentel, C.C.; Mechali, M.; May, P.; Kress, M. Oncogene 1, 71-78, 1987 A; Title: Cloning and characterization of a cDNA from Xenopus laevis codir A; Reference number: A29376; MUID:88143684 A; Reference number: A29376 A; MUID:88143684 A; References: EMBL:X05191; NID:964961; PIDN:CAA28821.1; PID:964962 A; Residues: 1-363 <SOU>
A; Cross-references: EMBL:X05191; NID:964961; PIDN:CAA28821.1; PID:964962 R; Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knoechel, W. Oncogene 9, 109-120, 1994 A; Title: Overexpression of Wild-type p53 interferes with normal developme A; Reference number: 151639; MUID:94134403 A; Accession: S61531 A; Molecule type: mRNA A; Residues: 1-293, 295-363 <HOE>
A; Residues: 1-293, 295-363 <HOE>
A; Residues: 1-293, 295-363 <HOE>
A; Residues: Data Library, March 1994
Submitted to the EMBL Data Library, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 LTANNAKMRESLLRSENPNSVYCGNAQGKGISE----RFSVVVPLNMSRSVTRSGLTRQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 LAFKFVCQNSCIG -- - RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQLNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKRKSVPEAAEEDEPSKVRRCIAIKTEDTESNDSRDCDDSAAEWNVSRTPDGDY-RLAIT
                                                                                                                                                                                                      R; Dequiedt, F.; Willems, L.; Burny, A.; Kettmann, R. submitted to the EMBL Data Library, September 1994
A; Description: Nucleotide sequence of the ovine p53 tumor-suppressor A; Reference number: S51648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 YSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCFS--NDVSAPVVRCQNHLSV
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                                                                                                           N;Alternate names: tumor-suppressor protein p53
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
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                                                                                      p53
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A; Status: preliminary
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                                                                                    cellular tumor
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QY 222 AFKFVCQNSCIGRKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQLNSK 278 ::: : : : : : : : : : : : : : : : : :	ને ા
JLT 5 824 [ular tumor an pecies: Mus mus te: 13-Jan-19 ccession: S388 rai, N.; Nomur Cell. Biol. itle: Immunolo eference numbe	lular tumor antigen p53 - m lternate names: oncoprotein pecies: Mus musculus (house ate: 28-Aug-1985 #sequence_ ccession: A22739; S06336; A ienz, B.; Zakut-Houri, R.; O J. 3, 2179-2183, 1984 itle: Analysis of the gene eference number: A22739; MU ccession: A22739 olecule type: DNA esidues: 1-134,'V',136-390
Discule type: esidues: 1-381 ross-reference an, K.A.; Kule leic Acids Res itle: Alternat eference numbe ccession: S354 catus: nucleic	A; Cross-references: GB: X00876; NID: 9871420; PIDN: CAA25420.1; PID: 9871421; GB: X01237; R; Chumakov, P.M. Bioorg. Khim. 13, 1691-1694, 1987 A; Title: Primary structure of DNA complementary to murine oncoprotein p53 mRNA. A; Reference number: S06336; MUID: 88221682 A; Reference number: S06336 A; Accession: S06336 A; Accession: S06336 A; Accession: S06336 A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-134, 'V', 136-390 <chu></chu>
ecule type: mRNA idues: 1-381 <han> ss-references: EMBL:M13874 e: the nucleotide sequence hent: This sequence, produ known. erfamily: cellular tumor a vords: alternative splicin VDomain: transcription ac</han>	7.7. (17.7.) (
5-26/Region: conserved region I 5-289/Domain: DNA-binding core #status predicted <- 18-121/Region: L1 loop 14-139/Region: conserved region II 50-192/Region: L2 loop 58-178/Region: conserved region III 31-252/Region: conserved region IV 33-248/Region: L3 loop 57-283/Region: conserved region V	ol. 6, 3232-3239, 1986 nologically distinct p53 mol umber: S38822; MUID:87064640 S38822 pe: mRNA -390 <ara1> ences: EMBL:M13872; NID:9200 S38823</ara1>
13-319/Region: nuclear location signal 19-357/Region: tetramer association 19.357/Region: tetramer association 19,18,23,37/Binding site: phosphate (Ser) (covalent) #stat 13,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #stat 12/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) 12/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase)	A 169 EMBL: Do.; Y S4001
Matches 72; Conservative 49; Mismatches 114; Indels 56; Gaps 14; QY 107 YSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCFSNDVSAPVVRCQNHLSVEP 164	Residues: 1-167 Cross-reference Jenkins, J.R.; cleic Acids Res Title: Cloning Reference numbe Accession: I487 Status: transla Molecule type: Residues: 1-47, Cross-reference Comment: This D Comment: This D

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Query Match
Best Local Similarity
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                                                                                                 281
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               mer; phosphoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleus; phosph
C; Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein F; 1-44/Domain: transcription activation #status predicted <TRA>
F; 16-26/Region: conserved region I
F; 99-289/Domain: DNA-binding core #status predicted <:,BC>
F; 108-121/Region: L1 loop
F; 114-139/Region: L2 loop
F; 160-192/Region: conserved region II
F; 233-248/Region: conserved region IV
F; 233-248/Region: conserved region IV
F; 233-248/Region: conserved region V
F; 313-319/Region: unclear location signal
F; 319-357/Region: tetramer association
F; 319-357/Region: tetramer association
F; 319-357/Region: tetramer (Ser) (CCV..Lent) #status predicted
F; 312/Binding site: phosphate (Ser) (covalent) #status predicted
F; 389/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oncoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Callular tumor antigen p53 - chicken
N.Alternate names: nuclear oncoprotein p53
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: $02193
R;Soussi, T.; Begue, A.; Kress, M.; Stehelin, D.; Mav, P.
Nucleic Acids Res. 16, 11383, 1988
A;Title: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprot A;Reference number: $02193; MUID:89083584
A;Reference number: $02193; MUID:89083584
A;Residues: 1-367 <Sou>
A;Residues: 1-367 <Sou>
A;Cross-references: EMBL:X13057; NID:963740; PIDN:CAA31456.1; PID:963741
C;Superfamily: cellular tumor antigen p53
C;Reywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus F;161,164,224,228/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 YSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF--SHDVSAPVVRCQNHLSVEP 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SNDVSAPVVRCQNHLSVEP 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTANNAKMRESLLRSENPNSVYCGNAQGKGISERFSVVVPLNMSRSVTRSGLTRQTLAFK 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 GTDGLAPAQHLIRVEGNPQARYHDDETTK----RHSVVVPY----EPPEVGSDCTTVLYN 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -EPPEAGSEYTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 LTANNAKMRESLLRSENPNSVYCGNAQGKGISE----RFSVVVPLNMSRSVTRSGLTRQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                                                                                                                                                               390;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GNLYPEYLEDROTFRHSVVVPY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                   95;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 168.5; DB 1;
Pred. No. 3.5e-06;
3; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,63
89;
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29.4%; Pred. No. 3.6e-06;
ive 29; Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --PPGSAKRALPTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
                                                                                                                                                                                                                                                                                                                                                                                                             8.4%; 25.6%;
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60; Conser
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Best Local
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tunor suppressor protein p53 - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 23-Jul-1999
C;Accession: JC6176
R;Lee, H; Larner, J.M.; Hamlin, J.L.
Gene 184, 177-183, 1997
A;Title: Cloning and characterization of Chinese hamster p53 cDNA.
A;Reference number: JC6176; MUID:97183659
A;Contents: liver
A;Reference number: JC6176
A;Molecule type: mRNA
A;Residues: 1-393 <LEE>
A;Contents: liver
A;Residues: 1-393 <LEE>
A;Cross-references: GB:U50395; NID:g1842229; PIDN:AAC53040.1; PID:g1842230
C;Comment: This protein is a multimer, it plays the central role in a complex DNA digenetics:
A;Genetics:
A;G
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R; Le Goas, F.; May, P.; Ronco, P.; de Fromentel, C.C.
Gene 185, 169-173, 1997
A; Title: cDNA cloning and immunological characterization of rabbit p53.
A; Reference number: JC6193; MUID: 97208869
A; Reference number: JC6193
A; Molecule type: mRNA
A; Residues: 1-391 < LEA>
A; Residues: 1-391 < LEA>
A; Residues: 1-391 < LEA>
A; Genetics:
A; Genetics:
A; Gene: p53
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C; Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
FVCQNSCIG---RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDR-IQDERQLNSKKR 280
                                                          107 YSIPLNKLYIRMNKAFNVDVQFKSKMP----IQPLNLRVFLCFSNDVSAPVVRCQNHLSV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 YSPSLNKLFCQLAKTCPVQLWVNSTPPPGTRVRAMAIYKKLQYMTEV---VRRCPHH--E 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 KRKSVPEAAEEDEPSKVRRCIAIKTEDTESNDSRDCDDSAAEWNVSRTPDGDY-RLAITC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
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Pred. No. 3.9e-06;
2; Mismatches 113
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                                                                                                                                                                                                                                                                                                         279 GGAGGVAKRAMSPPTEAPEPPKKR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                         -KSVPEAAEEDEPSKVR
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cellular tumor antigen p53 [validated] - human
N;Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppr
                                                                                                                                                                                                                          Species: Homo sapiens (man)
Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000
Accession: A25224; A43073; JT0436; S40773; S42669; A22837; A55060; A25397; B25397;
905; I58354; I78850; I52681; S60153
Lamb, P.; Crawford, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-393 <LAM>
A; Residues: 1-393 <LAM>
A; Cross-references: EMBL: X01405; GB:M13121; GB:N00032; NID:g189460; PIDN: AA59987.1; B; Buchman, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P. Gene 70, 245-252, 1988
A; Title: A variation in the structure of the protein-coding region of the human p53 (A); Reference number: JT0436; MUID:89108008
          263 VCACPGRDRKTEE--INLKKQQETTLETKTKPAQGIKRAM 300
                                                                                                                                                                                                                                                                                                                                                      R;Lamb, P.; Crawford, L.
Mol. Cell. Biol. 6, 1379-1385, 1986
A;Title: Characterization of the human p53 gene.
A;Reference number: A25224; MUID:87064416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A25224
A; Molecule type: DNA
A; Residues: 1-393 <LAM>
                                                                                                        RESULT
          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          callular tumor antigen p53 - rainbow trout
C; Species: Oncorhynchus mykiss (rainbow trout)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: JH0631
R; de Fromentel, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.
Gene 112, 241-245, 1992
A; Title: Rainbow trout p53: cDNA cloning and biochemical characterization.
A; Reference number: JH0631; MUID:92210006
A; Reference number: JH0631; MUID:92210006
A; Residues: 1-396 < CDEF>
A; Residues: 1-396 < CDEF
A; Residues: 1-399 < CDEF
A; Residues: 1-390 < CDEF
A; Residu
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                                                                                               Score 165.5; DB 2;
Pred. No. 6.2e-06;
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       antigen
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illarity 23.8%;
Conservative 5
     tumor
     cellular
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C;Keywords: tumor
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Similarity A; Molecule type: mRNA A; Residues: 1-253, 'D', 65; Query Match Best Local S Matches g g δλ ò <F01> A; Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line A; Accession: B25397
A; Molecule type: mRNA
A; Residues: 1-71,'P',73-78,'T',80-393 <HAR2>
A; Residues: 1-71,'P',73-78,'T',80-393 <HAR2>
A; Cross-references: EMBL:M14695; NID:g339815; PIDN:AAA61212.1; PID:g339816
A; Cross-references: clone p53-H-19, transformed hybridoma SV-80 cell line R; Matlashewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Schneider, J.; Crawford, L.V. Mol. Cell, Biol. 7, 961-963, 1987
A; Title: Primary structure polymorphism at amino acid residue 72 of human p53.
A; Reference number: S42452; MUID:87144273 A; Molecule type: mRNA A; Residues: 1-189, 'LLSILSEWKEICVWSIWMTETLFDIVWWCPMSRLRLALT', 'VPPSTTTTCVTVPAWAA' A; Cross-references: EMBL:X60010; NID:g506432; PIDN:CAA42625.1; PID:g506433 A; Note: deletion of a C nucleotide causes a frameshift at position 566 A; Accession: I38083 A; Status: translated from GB/EMBL/DDBJ 506447 506449 506435 506439 506443 506445 506437 506441 a polymorphism EMBO J. 10, 2879-2887, 1991
A; Title: p53 is frequently mutated in Burkitt's lymphoma cell lines.
A; Reference number: I38082; MUID:92007731
A; Accession: I38082
A; Accession: Lianslated from GB/EMBL/DDBJ PID:g PID:g PID:9 PID:9 PID:q PID:g PID:q PID:q A; Residues: 1-192. "R', 194-393 <F02>
A; Cross-references: EMBL:X60011; NID:9506434; PIDN:CAA42626.1; PID: A; Accession: 138084
A; Accession: 138084
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-393 <F03>
A; Cross-references: EMBL:X60012; NID:9506436; PIDN:CAA42627.1; PID: A; Accession: 138085
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-245, T', 247-393 <F04>
A; Cross-references: EMBL:X60013; NID:9506438; PIDN:CAA42628.1; PID: A; Accession: 138086
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-236, T', 238-393 <F05>
A; Cross-references: EMBL:X60014; NID:9506440; PIDN:CAA42629.1; PID: A; Accession: 138087
A; Residues: 1-247, 'Q', 249-393 <F05>
A; Cross-references: EMBL:X60015; NID:9506444; PIDN:CAA42630.1; PID: A; Molecule type: mRNA
A; Residues: 1-247, 'Q', 249-393 <F06>
A; Cross-references: EMBL:X60016; NID:9506444; PIDN:CAA42631.1; PID: A; Accession: 138088
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-71, 'Q', 249-393 <F08>
A; Cross-references: EMBL:X60017; NID:9506446; PIDN:CAA42632.1; PID: A; Accession: 138099
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-17, 'Q', 249-393 <F08>
A; Cross-references: EMBL:X60018; NID:9506446; PIDN:CAA42632.1; PID: A; Accession: 138099
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-21, 'P', 'J', 249-393 <F08>
A; Cross-references: EMBL:X60018; NID:9506446; PIDN:CAA42633.1; PID: A; Accession: 138099
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-212, 'Q', 214-393 <F10>
A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DBJ
A; Status: translated from GB/EMBL/DBJ
A; Status: translated from GB/EMBL/DBJ Crook, P.J.; Allan, G.J.; Shanahan, F.; Vousden, K.H.; , 2879-2887, 1991 represent to s was also found, and appears \$42453 lambda C113 A; Molecule type: mRNA; DNA A; Residues: 66-71, 'P', 73-79 <MKI2> A; Experimental source: clone lambda clone J6K mRNA 2,'R',194-393 DNA A; Residues: 66-79 < MKI3>
A; Experimental source: clo
R; Farrell, P.J.; Allar A; Molecule type: mRl A; Residues: 1-192, 'I A; Cross-references: S42452 A; Experimental A; Note: 72-Cys A; Accession:

OY 221 LAFKFVCQNSCIGRKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQLNS : :: : : : : :	CPKRDRIQDERQLNS 277	A;Map position: 4 A;Introns: 20/2; 118/2; 171/3; 251/2; 286/3; 315/1; 354/3; 410/3; 469/2; 506/1; 542/3 A;Note: F20M13.150 C;Superfamily: beta-galactosidase bga
Db 292 KSEPHHELPPGSTKRALPNNTSSSPQPKR QY 337 CPNKEWLLQSIEGMIKEAAAEVLRNPNQENLRRHANKLLSLK 378	::	Query Match Best Local Similarity 21.8%; Pred. No. 0.68; Matches 71; Conservative 53; Mismatches 116; Indels 86; Gaps 16;
34	m	QY 5 QPMSWHKESTDSEDDSTEVDIKEDIPKTVEVSGSELTTEPMAFLQGLNSGNLMQFSQQSV 64 : :: :
tumor an tumor an s: Cercop 10-Sep-19 ion: S065 Acids Res Acids Res Acids Res Nucleoti nce numbe	change 10-Sep-1999	65 LREMMLQDIQIQANTLPKLENH
lues: 1-393 <rig> lues: EMBL:X16384; NID:g22795; PIDN:CAA344 leamily: cellular tumor antigen p53 lues: apoptosis; cell division control; DNA binding ords: apoptosis; cell division control; DNA binding 179,238,242/Binding site: zinc (Cys, His, Cys, Cys) linding site: phosphoryl-RNA (Ser) (covalent) #sta</rig></rig></rig></rig></rig></rig></rig>	120.1; PID:g22796 ng; homotetramer; nucleus; phosph s) #status predicted	QY 235 KETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQLNSKKRKSVPEAAEED 290
Query Match Best Local Similarity 22.7%; Pred. No. 8e-05; Matches 64; Conservative 50; Mismatches 124; In	Length 393; Indels 44; Gaps 11;	Db 839 EDDDEEEEEEDKENKDTKDMEN 860 RESULT 14
QY 107 YSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCFSNDVSAPVVRCQNHLSVE 	SNDVSAPVVRCQNHLSVEP 164 :: : SQHMTEVVRRCPHHERCS- 183	<pre>rrsor [validated] glycoprotein; li lus (chicken)</pre>
OY 165 LTANNAKMRESLLRSENPNSVYCGNAQGKGISERFSVVVPLNMSRS:::::::::::::::::::::::::::::::::::	MMSRSVTRSGLTRQT 220 EPPEVGSDCTT 231	sequence_revision 18-Aug-200 S55680; A92941; A93502; C291 net Schip, F.D.; Gerber-Huber 15377-15385, 1987
QY 221 LAFKFVCQNSCIGRKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQLNS : :: : : : : : : : :	OPKRDRIQDERQLNS 277	of the orga [50441; MU] /; translat
	EWNVSRTPDGDY-RLAIT 336 : : PQPKKKPLDGEYFTLQIR 333 378	A; Residues: 1-1852 <nar> A; Residues: 1-1852 <nar> A; Cross-references: GB:M18060; NID:g212880; PIDN:AAA49139.1; PID:g212881 R; Yamamura, J.; Adachi, T.; Aoki, N.; Nakajima, H.; Nakamura, R.; Matsuda, T. Biochim. Biophys. Acta 1244, 384-394, 1995 A; Title: Precursor-product relationship between chicken vitellogenin and the yolk pro</nar></nar>
Db 334 GRERFEMFRELNEALELKDÄQAGKEPAGSRAHSSHLKŠKK 373 RESULT 13	σ.	A; Reference number: S55680; MUID: 95322425 A: Reference number: S55680 A; Reference number: S55680 A; Reference number: S55680 A; Reference number: S55680 A; Reference number: S55680; MUID: 95322425
alactosidase homolog F20M13.150 - Arabidopsis thal ies: Arabidopsis thaliana (mouse-ear cress): 23-Apr-1999 #sequence_revision 23-Apr-1999 #text ssion: T05687 n, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancr	liana t_change 02-Sep-2000 roft, I.; Mewes, H.W.; Mayer, K.E	Residues: 1569- van het Schip, Mol. Biol. 196 Title: Nucleoti Reference numbe Accession: A929
ted to the Florein Sequence Database, Febluary 133 erence number: 215420 ession: T05687 ecule type: DNA iques: 1-1036 <bev></bev>	7).	A; Molecule type: DNA A; Residues: 1-579,582-774,'R',776-1138,'S',1140-1437,'HK',1440-1852 <van> A; Residues: 1-579,582-774,'R',776-1138,'S',1140-1437,'HK',1440-1852 <van> A; Cross-references: GB:X13607; NID:g63886; PIDN:CAA31942.1; PID:g63887 A; Note: 1842-Ala was also found B; Dinch</van></van>
ss-references: EMB erimental source: etics:	M13	Nucleic Acids Res. 12, 1117-1135, 1984 Nucleic Acids Res. 12, 1117-1135, 1984 A; Title: Identification and sequence analysis of the 5' end of the major chicken vite A; Reference number: A93502; MUID:84118805

-KTEDTESNDSR

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Dybothetical protein T23K23.12 [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: D96703
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001
C; Accession: D96703
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 1616-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-314 <STO>
A; Residues: 1-314 <STO>
A; Residues: 1-314 <STO>
A; Genetics:
A; Map position: 1
A; Map position: 1
                                                                                                                                                              1118 TEPDAKTSSSSSASSTATSSASSSASSPNRKKPMDEEENDQVKQARNKDASSSSRSSKS 1177
                  226 VCQNSCIGRKETSLVFCLEKACGDIVGQH----VIHVKICTCPKRDRIQDERQLNSKKRKS 282
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                                                                                                                                                                                                                                           ---DCDDSAAEWNVSRTPDGDYRLAITCPNKEWLL-----QSIEGMIKEAAAEVLRNPN
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                                                                           A; Residues: 1.71 c888.
A; Cross-references: GB:XO345; NID:g63872; PIDN:CAA25096.1; PID:g63873
A; Cross-references: GB:XO345; NID:g63872; PIDN:CAA25096.1; PID:g63873
Int. J. Biochem. 17, 983-988, 1985
A; Title: The Primary structure of savian phosvitins. Contributions through A; Reference number: A31754; MUID:8605631
A; Accession: C25184
A; Accession: B. M.; van Her Schip, A.D.; van de Klundert, J.A.
B; A; Accession: L50440
A; Residues: 1150440
A; Residues: 1050440
A; Residues: 105040
A; Res
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1.5;
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llarity 19.6%; Pred. No. Conservative 71; Mismatcl
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A; Accession: A93502
A; Molecule type: DNA
                                                                     A;Residues: 1-71 <BU
A;Cross-references:
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-KPGAPGLTKWNLQ 125

Gaps

101;

Indels

:66

Length 314;

DB 2;

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Search completed: November 16, 2001, 15:50:51 Job time: 2443 sec

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pdates/sec
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2008
1 MYISQPMSWHKESTDSEDDS.....NLRRHANKLLSLKKRAYELP 385
                                                                                                          November 16, 2001, 15:49:08; Search time 32.01 Seconds (without alignments)
412.008 Million cell update
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Descripti	057538 xiphophorus 092143 xiphophorus 015350 homo sapien 09xsk8 cercopithec 029537 canis famil P10361 rattus norv P41685 felis silve 012946 platichthys 029628 bos taurus 09w679 tetraodon m P07193 xenopus lae 09w679 tetraodon m P07193 canis scrofa 000366 mesocricetu 093379 ictalurus p P79892 equus cabal 09w678 barbus barb P02340 mus musculu 064662 spermophilu P10360 gallus gall 009185 cricetulus 029480 equus asinu P51664 ovis aries 039wur6 cavia porce P51664 ovis aries 036006 marmota mon 095330 oryctolagus P79820 oryzias lat 09wur6 cavia porce P25035 oncorhynchu P04637 homo sapien P13481 cercopithec 09ttal tupaia glis P56423 macaca mula
SUMMAI	P53_XIPHA P73_KIPHA P73_KIPHA P73_KIPHA P53_XIPHA P53_KAT P53_RAT P53_RAT P53_RAT P53_BOVIN P53_PLAFE P53_BOVIN P53_BOVIN P53_BOVIN P53_BOVIN P53_BARBU
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P02845 gallus gall	Q02447 homo sapien
O02482 caenorhabdi	Q09441 caenorhabdi
P54623 drosophila	Q08787 bacillus su
P26802 drosophila	Q13201 homo sapien
O95613 homo sapien	P45577 escherichia
P45387 haemophilus	P53804 homo sapien
VIT2_CHICK	SP3_HUMAN
UN37_CAEEL	YP83_CAEEL
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8888888	4 4 4 4 4
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ALIGNMENTS

RESULT P53_XIPHE 1D P53_ AC 0575 DT 01-0 DT 01
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-!-FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.

APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2 EXPRESSION (BY SIMILARITY).

-:- SUBGNITT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
     OLIGOMERIZATION.
BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
87E4AE8CFAEE333D CRC64;
                                                                                                                                                                                                                                                            212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xiphophorus maculatus (Southern platyfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Poeciliidae; Xiphophorus.
                                                                                                                                                                                                           ESLAPPEGLLSQNMDFWEDPETMQE -- TKNVP-TAPTVPAISNY-AGEHGFNLEFNDSGT
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                                                                                                                                                                                                                                                                                                       NHLSVEPLTANNA --- KMRESLLRS -- ENPNSVYCGNAQGKGISERFSVVVPLNMSRSVT
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                                                                                                                                                                                                                                                                                                                                                                                       101 PKSLW-MYSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF--SNDVSAPVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and comparative sequence analysis of TP53 in xiphophoruhybrid melanoma models."; Gene 212:31-38(1998).
                                                                                                                                                                              EPMAFLQGLNSGNLMQFSQQSVLREMMLQDIQIQANTLPKLENHNIGGYCFSMVLDE-
                                                                                                                                                  42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=RIO JAMAPA / JP 163 A;
MEDLINE=98326307; PubMed=9661661;
Kazianis S., Gan L., Della Coletta L., Santi B., Morizot D.C.,
                                                                                                                                                                                                                                                                                                                                       -TRRHSVTVPYER-
                                                                                                                                                  Indels
                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 TEEGNLEKSGTKOTKKRKSAP-APDTSTAKKSKSASSGEDEDKE
                                                                                                                                                                                                                                                                                                                                                                                                                               --NSKKRKSVPEAAEEDEPSKVRRCIAIKTEDTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P53)
                                                                                                                                               112;
                                                                                                                Score 201; DB 1;
Pred. No. 2.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P53_XIPMA STANDARD; PRT; 342 AA. Q92143; 01-0CT-2000 (Rel. 40, Last sequence update) 01-0CT-2000 (Rel. 40, Last annotation update) 01-0CT-2000 (Rel. 40, Last annotation update) CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR
                                                                                                                                ed. No. 2.2e
Mismatches
                                                                                                                                                                                                                                                                                                                          :| | | | : | : | | | | : | | | | HQS-EDLSDNKSHLIRVEGSQLAQYFEDPN-
                                                                                                                                              53;
                                                                  MW;
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                                                                                                                 10.0%;
                                                                                                                                 27.18;
     317
336
281
341
37947
                                                                                                                                               Conservative
                                                                     AA;
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288
319
268
341
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                                                                                                                    Local Sim.
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    DOMAIN
DOMAIN
DOMAIN
MOD_RES
                                                                                                                 Query Match
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                                                                                                                                              Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 QGLNSGNLMQFSQQSVLREMMLQDIQIQANTLPKLENHNIGGYCFSMVLDE--PPKSLW- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF--SNDVSAPVVRCQNHLSVE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                  BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 EGLLSQNMDFWEDPETMQE--TKNVP-TAPTVPAISNY-AGEHGFNLEFNDSGTAKSVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 PLTANNA---KMRESLLRS--ENPNSVYCGNAQGKGISERFSVVVPLNMSRSVTRSGLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -TRRHSVTVPYER-----POLGSEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 QTLAFKFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 TYSVKLGKLFCQLAKTTPIGVLVKEEPP-QGAVIRATAVYKKTEHVGEVVKRCPHHQS-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 TILLSFMCNSSCMGGMNRRPILTILTLETTEGEVLGRRCFEVRVCACPGRDRKTEEGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                               Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
PROSITE; PS00348; P53; 1.
Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                            Nuclear protein; Phosphorylation; Apoptosis.

DOMAIN 1 35 TRANSCRIPTION ACTIVATION (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P73_HUMAN STANDARD; PRT; 636 AA.
015350; 015351; Q9NTK8;
01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
TUMOR PROTEIN P73 (P53-LIKE TRANSCRIPTION FACTOR) (P53-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   290739636108CEA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 199; DB 1; L
Pred. No. 3.2e-09;
2: Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 EKSGTKQTKKRKSAP-APDTSTAKKSKSASSGEDEDKE 289
                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY. OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A. (ISOFORMS ALPHA AND BETA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- NSKKRKSVPEAAEEDEPSKVRRCIAIKTEDTE
 SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 DLSDNKSHLIRVEGSQLAQYFEDPN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Colon;
MEDLINE=97433090; PubMed=9288759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
                                                                                                                                                            EMBL; AF043947; AAC31134.1; -. EMBL; AF043948; AAC26190.1; -.
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ilarity 27.0%;
Conservative 5
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P04637; ITSR.
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317
336
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                                                                                                                                                                                                                                                                                                                                                                                                                                  342 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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268
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SEQUENCE
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Best Local
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P73_HUMAN
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MEDLINE=99380160; PubMed=10449409;

Chi S.W., Ayed A., Arrowsmith C.H.;

"Solution structure of a conserved C-terminal domain of p73 with structural homology to the SAM domain.";

EMBO J. 18:4438-4445(1999).

-!- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE. WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d zeta.
Chalon P., Lelias J.-M., Dumont X., Ferrara P., McKeon
                                    Ç
                                                                                                                           McMenamin M.G., Hagiwara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Melino
                                                                                                                                                            in human cancer cell lines
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99021697; PubMed=9802988;
De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco Annicchiarico-Petruzzelli M., Levrero M., Melino G.;
"Two new p73 splice variants, gamma and delta, with different transcriptional activity.";
J. Exp. Med. 188:1763-1768(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sun X., Gu J., Huang Y., Lu
                                                 cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (ISOFORMS ALPHA AND BETA).
MEDLINE=99318135; PubMed=10391251;
Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., L
Kharbanda S., Weichselbaum R., Kufe D.;
"p73 is regulated by tyrosine kinase c-Abl in the apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sun X., Gu J., Huang Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Terrinoni A., Corazzari M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN.
SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS
                                                                                                                                                                                                                                            S., Alderete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           De Laurenzi V., Catani M.V., Terrinoni A., Corazzari M., Costanzo A., Levrero M., Knight R.A.;
"Additional complexity in p73: induction by mitogens in and identification of two new splicing variants epsilon Cell Death Differ. 6:389-390(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
                                at 1p36,
                                                                                                                                                                                                                     MEDLINE=98389621; PubMed=9721206; Mai M., Huang H., Reed C., Qian C., Smith J S., Alderet Jenkins R., Smith D.I., Liu W.; "Genomic organization and mutation analysis of p73 in oligodendrogliomas with chromosome 1 p-arm deletions." Genomics 51:359-363(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA).
TISSUE=Lymphocytes, Breast cancer, Hepatoma, and Skin;
MEDLINE=99310938; PubMed=10381648;
                               pressed gene related to p53 at 1p in neuroblastoma and other human
                                                                                                                                                                                                                                                                                                                                       (ISOFORMS GAMMA AND DELTA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yuan Z.-M., Shioya H., Ishiko T., Sun X
Kharbanda S., Weichselbaum R., Kufe D.;
Nature 400:792-792(1999).
                                                                                            SEQUENCE FROM N.A. (ISOFORM ALPHA).
MEDLINE=99289209; PubMed=10362363;
Yoshikawa H., Nagashima M., Khan M.A.,
Harris C.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaelin W.G. Jr.;
"The emerging p53 gene family.";
J. Natl. Cancer Inst. 91:594-598(1999)
                                                                                                                                                           "Mutational analysis of p73 and p53 Oncogene 18:3415-3421(1999).
                                                                                                                                                                                                          (ISOFORM ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISOFORM KAPPA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99217940; PubMed=10203277
                            "Monoallelically expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to DNA damage.";
Nature 399:814-817(1999).
                                             frequently deleted in cell 90:809-819(1997).
                                                                                                                                                                                                                                                                                                                                                      TISSUE=Neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                         "Mutational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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[10]
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                                                                                                                                                                                                                                                                                                                                                                                                                                             DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN NEUROBLASTOMA AND OLIGODENDROGLIOMA.

SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                               GAMMA,
                                                                                                                                                                                                                                                                                                                 SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
INDUCTION: NOT INDUCED BY DNA DAMAGE.
DOMAIN: POSSESES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS TO THE ABL TYROSINE KINASE SH3 DOMAIN.
TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: 7 ISOFORMS; ALPHA (SHOWN HERE), BETA, GAMMA DELTA, EPSILON, ZETA AND KAPPA; ARE PRODUCED BY ALTERNATIVE SPLICING OF EXON 11 IN GAMMA AND EPSILON ISOFORMS RESULTS IN A FRAMESHIFT FROM THE ORIGINAL READING FRAME. THE SPLICING OF EXON 13 IN EPSILON ISOFORM REVERTS THE READING FRAME
                                                                                                                                                                                                                                                                                                     HEART, LIVER,
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ASP/GLU-RICH (ACIDIC).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
MEDIATES OLIGOMERIZATION (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00348; P53; 1.
Transcription regulation; Activator; DNA-binding; Anti-oncogene
                                                                                                                                                                                                                                                                                                 KIDNEY, PLACENTA, COLON, HE ROSTATE, THYMUS AND PANCREAS
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TISSUE SPECIFICITY: BRAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00870; P53; 1.
3; PR00386; P53SUPPRESSR.
EE; PS00348; P53; 1.
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AAD39696.1;
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Y11416; CAA72221.1;
Y11416; CAA72219.1;
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                                PHOSPHORYLATION (BY ABL; ISOFORM BETA).

G -> GNTRCRHWVLCGDRGLSRPVLQGPSG (IN
ISOFORM KAPPA).

SFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPE
QYRMTIWRGLQDLKQGHDYSTAQQLLRSSNAATISIGGSGE
LQRQRVMEAVHFRVRHTITIPNRGGPGGPDEWADFGFDLP
DCKARKQPIKEEFTEAEIH -> RTWGP (IN ISOFORM
BETA).
                                                                                                                        SHLQPPSYGPVLSPMNKVHGGMNTLPSVNQLVGQPPPHSSA
ATPNLGPVGPGMLNNHGHAVPANGEMSSTHSAQSMV -> P
RDAQQPWPRSASQQRRDEQQPQRPVHGLGVPLHSATPLPRR
PQPRQFFNRIGVSKLHRVFHLPRVTEHLPPAEPDH (IN
ISOFORM GAMMA),
                                                                                                                                                                               MISSING (IN ISOFORM GAMMA).
SHLQ -> TWGP (IN ISOFORM DELTA).
MISSING (IN ISOFORM DELTA).
SHLQPPSYGPVLSPMNKVHGGMNKLPSVNQLVGQPPPHSSA
                                                                                                                                                                                                                              VHGLGVP
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LHSATPLPRRPQPR (IN ISOFORM EPSILON)
MISSING (IN ISOFOR / EPSILON).
MISSING (IN ISOFORM ZETA).
A467493C5D93EEE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                WMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQP-LNLRVFLCF--SNDVSAPVVRCQNHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEPLTANNAKMRESLLRSENPN-SVYCGNAQGKGISERFSVVVI-LNMSRSVTRSGLTR(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom.
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                        SPYTPEHAASVPTHSPYAQPSSTFDTMSPAPVIPSNTDYP-GPHHFEVTFQQSSTAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - EPPQVGTEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 40, Created)
.. 40, Last sequence update)
.. 40, Last annotation update)
?? (P53-LIKE TRANSCRIPTION FACTOR) (P53-RELATED
                                                                                                                                                                                                                                                                                                                                  58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCPKRDRIQDE-
                                                                                                                                                                                                                                                                                                                                                      EDDSTEVDIKEDIPKTVEVSGSELTTEPMAFLQGLNSGNLMQFSQQSVLREMMLQ-
                                                                                                                                                                                                                                                                                                            Length 636;
                                                                                                                                                                                                                                                                                                                                                                                                    --DIQIQANTLPKLENHNIGGYCFSMVLDE-
                                                                                                                                                                                                                                                                                                                                 Indels
                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -VTGRQSVVVPY--
                                                                                                                                                                                                                                                                                                       ; DB 1; L
3.5e-08;
ches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAFKFVCQNSCIG - - - RKETSLVFCLEKACGDIVGQHVIHVK :
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                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 637
                       -BINDING
                                                                                                                                                                                                                                                                                                          Score 191;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRDFNEGQSAPASHLIRVEGNNLSQYVDDP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -RQLN--SKKRKSVPEAAEEDEPSKV 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQALNESSAKNGAASKRAFKQSPPAV
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394
486
310
99
282
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403
636
445
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495
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78; Conserv
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Q9XSK8; Q9TSQ9;
01-OCT-2000 (Rel, 4
01-OCT-2000 (Rel, 4
01-OCT-2000 (Rel, 4
TUMOR PROTEIN P73 (
                                                                                                                                                                                                                                                                       636 AA;
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NCBI_TaxID=9534;
391
483
131
99
282
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400
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 DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation; Activator; DNA-binding; Anti-oncogene;
Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing.
VARSPLIC 495 637 SFLTGLGCPNCIEYFTSQGLQSIXHLQNLTIEDLGALKIPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QYRMTIWRGLQDLKQGHDYGAAAQQLLRSSNAAAISIGGSG
ELQRQRVMEAVHFRVRHTITIPNRGGPGAGPDEWADFGFDL
PDCKARKQPIKEEFTEAEIH -> RTWGP (IN ISOFORM
                                                                                                                                                                                                                         TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT.
SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA;
ARE PRODUCED BY ALTERNATIVE SPLICING.
DOMAIN: POSSESES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS TO THE ABL TYROSINE KINASE SH3 DOMAIN.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                         TO DNA DAMAGE P53-RESPONSIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPDSTYFDLPQSSRGNNEVVGGTDSSMDVFHLEGMTTSVMAQFNLLSSTMDQMSSRAASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -DIQIQANTLPKLENHNIGGYCFSMVLDE---PPKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 SPYTPEHAASVPTHSPYAQPSSTFDTMSPAPVIPSNTDYP-GPHHFEVTFQQSSTAKSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 WMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQP-LNLRVFLCF--SNDVSAPVVRCQNHLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WTYSPLLKKLYCQIAK - - TCPIQIKVSAPPPPGTAIRAMPVYKKAEHVTDIVKRCPNHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEPLTANNAKMRESLLRSENPN-SVYCGNAQGKGISERFSVVVPLNMSRSVTRSGLTRQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 GRDFNEGQSAPASHLIRVEGNNLSQYVDDP----VTGRQSVVVPY----EPPQVGTEFTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 EDDSTEVDIKEDIPKTVEVSGSELTTEPMAFLQGLNSGNLMQFSQQSVLREMMLQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58
58
                                                                                                                                                    MAY BE A TUMOR SUPPRESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 637;
                                                                                                                                                                         PROTEIN (BY SIMILARITY).
SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                  databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7CB200B919C9C70A CRC64;
                                                       Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databas -- I - FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; DB 1;
4.2e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 190;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y11419; CAA72224.1; ...
EMBL; Y11419; CAA72225.1; -..
HSSP; P04637; 1YCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            637 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
TISSUE=Kidney;
                                                                                                                                                                                                       SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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12;

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P53_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDUCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kraegel S.A., Pazzi K.A., Madewell B.R.;

"Sequence analysis of canine p53 in the region of exons 3-8.";

Cancer Lett. 92:181-186(1995).

-!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCE GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL

CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.

APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ishizaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR.
DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
IN MANY TYPES OF CANCER.
                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                Euteleostomi;
Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Spleen;
Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishiz
Watari T., Hasagawa A., Tsujimoto H.;
"Aberrations of p53 tumor suppressor gene in various spontaneou tumors in the dog.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Activator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                       "Isolation of canine p53 cDNA and detailed characterization full length canine p53 protein."; Oncogene 16:1077-1084(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NA-binding; Transcription regulation;
Phosphorylation; Apoptosis.
44 TRANSCRIPTION ACTIVATION
                                                                                                                                                     Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebreta;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REPRESSION
P53_CANFA STANDARD; PRT; 381 AA. Q29537; Q9TV78; 01-NOV-1997 (Rel. 35, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) CELEULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASIC
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Leukocyte;
MEDLINE=98178696; PubMed=9519881;
Veldhoen N., Milner J.;
"Isolation of canine p53 cDNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BEAGLE;
MEDLINE=95323915; PubMed=7600529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF060514; AAC16909.1; -.
EMBL; AB020761; BAA78379.1; -.
EMBL; S77819; AAB42022.1; -.
HSSP; P04637; 1YCS.
InterPro; IPR002117; -.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
PROSITE; PS00348; P53; 1.
Anti-oncogene; DNA-binding; Trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF 25-300 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280
344
375
                                                                                                                                                                                                                        NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89
313
356
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HHHEE RANKER REPRESENCE CON CONTROLL RESERVER RESERVER REPRESENT FOR THE PROPERTIES OF THE PROPERTIES

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                                                                                                                                                                                                                                                                                                                          111 WTYSPLLNKLFCQLAKTCPVQLWVSSPPPPNTC-VRAMAIYKKSEFVTEVVRRCPHHERC 169
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Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES. APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2 EXPRESSION.
    (POTENTIAL).
                                                                                                                                                                                                                                  Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                          163 EPLTANNAKMRESLLRSENPNSVYCGNAQGKGISE----RFSVVVPLNMSRSVTRSGLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 TTIHYNYMCNSSCMGGMNRRPILTITLEDSSGNVLGRNSFEVRVCACPGRDRRTEEENF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 QTLAFKFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- DGEY ----
                                                                                                                                                                                                                                63;
                                                                                                                                                                              Length 381;
                            PHOSPHORYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soussi T.;
"Nucleotide sequence of a cDNA encoding the rat p53 nuclear
                                                                                                                                                                                                                                 Indels
    NUCLEAR LOCALIZATION SIGNAL
                                                                                               761A718FDC93DA59 CRC64;
                                                 -> QEP (IN REF. 2).
P (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hulla J.E., Schneider R.P.; "Structure of the rat p53 tumor suppressor gene."; Nucleic Acids Res. 21:713-717(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1989 (Re' 10, Created)
01-MAR-1989 (Re 10, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - IRGRERY EMFRNINEALELK
                                                                                                                                                                          Score 183.5; DB 1
Pred. No. 7.1e-08;
15; Mismatches 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 HKK----GEPCPEPPGSTKRALPPSTSSSPPOKKKPL-
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                                                  EES
                                                                                                                                                                                                                           45;
                                                                                               42486 MW;
                                                                                                                                                                         9.1%;
                                                                                                                                                                                                                          Conservative
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\begin{array}{c} 311 \\ 380 \end{array}
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                                                                                               381 AA;
                                                                                                                                                                                                     Similarity
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P10361; 009168;
01-MAR-1989 (Re)
299
380
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                      MOD_RES
CONFLICT
                                                                                              SEQUENCE
                                                                                                                                                                          Query Match
                                                                       CONFLICT
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 DOMAIN
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OR TRP53.
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                                    Mammalia;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
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                                 INACTIVATED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DGDGLAPPQHLIRVEGNPYAEYLDDRQ----TFRHSVVVPY----EPPEVGSDYTTIHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSISLNKLFCQLAKTCPVQLWVTSTPP-PGTRVRAMAIYKKSQHMTEVVRRCPHHERCS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KFVCQNSCIG - - - RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQLNSKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.

OLIGOMERIZATION.

BASIC (REPRESSION OF DNA-BINDING).

NUCLEAR LOCALIZATION SIGNAL (POTENT PHOSPHORYLATION (BY SIMILARITY).

G -> S.
                      VARIET
                                                                                                                                                                                                                                                                                                                  Activator
                                                                                                                                                                                                                                                                                                                                       (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 391;
 (BY SIMILARITY)
                      WIDE
OR IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                         ion; Apoptosis.
TRANSCRIPTION ACTIVATION
                                                                                                                                                                                                                                                                                                                  regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                    -> W (IN REF. 2).
E62522313A5C872F CRC64
                     NTS IN A
MUTATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              annotation update) (TUMOR SUPPRESSOR P53)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 183; DB 1;
Pred. No. 8.1e-08;
                   IS FOUND IN INCREASED AMOUNTS ED CELLS. P53 IS FREQUENTLY MUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               315
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995 (Rel. 32, Last sequence update)
000 (Rel. 40, Last annotation update)
TUMOR ANTIGEN P53 (TUMOR SUPPRESSO
                                                                                                                                                                                                                                                                                                   PROSITE; PS00348; P53; 1.
Anti-oncogene; DNA-binding; Transcription
Nuclear protein; Phosphorylation; Apoptosi
DOMAIN
1 47
TRANSCRIPTION
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 BINDS DNA AS AN HOMOTETRAMER
                                                   SIMILARITY: BELONGS TO THE P53 FAMILY
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           NUCLEAR.
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                                                                                                                                                                                                                                                                                          P53SUPPRESSR
                                                                                                                                                                                                                                                                                                                                                                                                                             43451 MW;
                            OF TRANSFORMED CELLS. PS
IN MANY TYPES OF CANCER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.18;
nilarity 27.08;
Conservative 3
                                                                                                                                                      EMBL; X13058; CAA31457.1; EMBL; L07910; AAA41788.1; EMBL; L07904; AAA41788.1; EMBL; L07905; AAA41788.1; JEMBL; L07906; AAA41788.1; JEMBL; L07908; AAA41788.1; JEMBL; L07909; AAA41788.1; JEMBL; S02192; S02192.
SUBUNIT: BINDS DNA AS
SUBCELLULAR LOCATION:
DISEASE: P53 IS FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                             290
3954
321
390
103
174
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P04637; 1PET.
Pro; IPR002117;
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323
366
309
390
103
174
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P41685;
01-NOV-1995
01-NOV-1995
01-OCT-2000
CELLULAR TUMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58;
                                                                                                                                                                                                                                                                        InterPro;
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VARIANT
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Matches
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MEDLINE=94114699; PubMed=8286534;

A Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watari T., Goitsuka R.,

O'Brien S.J., Tsujimoto H., Hasegawa A.;

Molecular cloning and chromosomal mapping of feline p53 tumor

T suppressor gene.";

J. Vet. Med. Sci. 55:801-805(1993).

C -: FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES

GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL

CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN

TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-

C ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY

CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE

CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS.

APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF

BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                   Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y., Youn H.Y., Watari T., Goitsuka R., Tsujimoto H., Hasegawa A.; "Cloning of feline p53 tumor-suppressor gene and its aberration in hematopoietic tumors."; Int. J. Cancer 58:602-607(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: NUCLEAR.
DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
                                                             Euteleostomi;
Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61;
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TRANSCRIPTION ACTIVATION (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                           Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106;
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D08B43BA1BC8EB78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OLIGOMERIZATION.
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Mismatches
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SIMILARITY: BELONGS TO THE P53 FAMILY.
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                                                                                                                                                                                                                                                                                                                                     PubMed=8056458;
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Nuclear protein; Phosphorylation;
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EMBL; D16460; BAA03927.1; -.
HSSP; P04637; 1SAH.
InterPro; IPR002117; -.
Pfam; PF00870; P53; 1.
Felis silvestris catus (Cat).
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285
                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94
318
361
304
385
285
386 AA;
                                                                                                                                                                                                                                                                          TISSUE-Lymph node;
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                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                          MEDLINE=94333960;
                                                                                                                                            NCBI_TaxID=9685;
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collaboration
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COMP. Biochem. Physiol. 121B:235-242(1998).

-1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL.

CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANSACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES. APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2 EXPRESSION (BY SIMILARITY).
 218
                                                                       275
                                                                                                                                              335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Platichthys flesus (European flounder).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;

Pleuronectoidei; Pleuronectidae; Platichthys.
 --- RFSVVVPLNMSRSVTRSGLTR
                                                                    QTLAFKFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQL
                                 --EPPEVGSDC
                                                                                                           NF
                                                                                                                                          NSKKRKSVPEAAEEDEPSKVRRCIAIKTEDTESNDSRDCDDSAAEWNVSRTPDGDYRLAI
                                                                                       Anti-oncogene; DNA-binding; Transcription regulation; Activator Nuclear protein; Phosphorylation; Apoptosis.
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                                                                                                                                                                 ||:|
--DGEY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cachot J., Galgani F., Vincent F.; control of flounder p53 tumour
                              -- GNLHAKYLDDRNTFRHSVVVPY
                                                                                                                                                                                                                                                                                                                                                                                                                                     P53)
                                                                                                                                                                                                                TCPNKEWLLQSIEGMIKEAAAEVLRNPNQENLRRHANKLLSLK
                                                                                                                                                                                                                                                      - IRGRERFEMFRELNEALELK
                                                                                                                                                                           ---GEPCPEPPPGSTKRALPPSTSSTPPQKKKPL--
                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR)
TP53 OR P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
OLIGOMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: NUCLEAR. SIMILARITY: BELONGS TO THE P53 FAMILY.
EPLTANNAKMRESLLRSENPNSVYCGNAQGKGISE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=9972298
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PRINTS; PR00386; P53SUPPRESSR.
PROSITE; PS00348; P53; 1.
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                                                                                                                                                                                                                                                                                                                                              STANDARD;
                  -PDSSDGLAPPQHLIRVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13/; 11CS.
IPR002117;
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Biochem. Phy
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                                                                                                                                                                             RKK--
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                                                                                                                                                                                                                                                                                                                                            P53_PLAFE
O12946;
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Bishop R.R.P., Gobright E.E.I.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANSACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
                                                                                                                                                                                                                                                                                                                        Gaps
                                         NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                taurus (Bovine), and Bos indicus (Zebu).
Tyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Talia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | : |: | : | |: | : | : | | | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 PLTANNAKMRESLLRSE-NPNSVYCGNAQGKGISERFSVVVPLNMSRSVTRSGLTRQTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 NGPKQTKKRKQAPSNSAPHTTTVMKSKSSSAEEEDKEVFTVLVKGRERYEIIKKINEAF
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SEQUENCE FROM N.A.
SPECIES=Bovine; TISSUE=Liver;
MEDLINE=95352829; PubMed=7626789;
Dequiedt F., Kettmann R., Burny A., Willems L.;
"Nucleotide sequence of the bovine P53 tumor-suppressor cDNA.";
                                                                                                                                                                                                                                                                                                                      82;
    BASIC (REPRESSION OF DNA-BINDING)
                                                                              PHOSPHORYLATION (BY SIMILARITY). 4 0DE4CA20B22BB88 CRC64;
                                                                                                                                                                                                                                              Length 366;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
                                                                                                                                                                                                                                                                                                               109;
                                                                                                                                                                                                                                     Score 181; DB 1;
Pred. No. 1.1e-07;
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                                                                                                               40619 MW;
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                                                                                                                                                                                                                                   9.0%;
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                                                                                                               366 AA;
                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
CONTROLLING A SET OF GENES REQUIRED FUR THIS FROCESS. ONE SET ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES. APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARIA.
OLIGOMERIZATION.
BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
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                                                                                                                                                                                                                                          OR INACTIVA
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DOMAIN

1 44 TRANSCRIPTION ACTIVATION (ACIDIC).

DOMAIN

318 349 OLIGOMERIZATION.

DOMAIN

361 380 BASIC (REPRESSION OF DNA-BINDING).

DOMAIN

304 316 NUCLEAR LOCALIZATION SIGNAL (POTEN NUCLEAR SIGNAL (POTEN NUCLEAR SIGNAL (POTEN SIGNAL).

CONFLICT

380 380 R -> T (IN REF. 2).
                                                                                                                                                        (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regulation;
                                                                                                                                            SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILA SUBCELLULAR LOCATION: NUCLEAR.
DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED IN MANY TYPES OF CANCER.
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Pred. No. 1.3e-07;
); Mismatches 120;
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Conservative 50;
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PF00870; P53;
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386 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                           Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;

"Evolutionary conservancy of p53 gene sequences in fish.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.

APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
PHOSPHORYLATION (BY SIMILARITY).
                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 LTANNAKMRESLLRSE-NPNSVYCGNAQGKGISERFSVVVPLNMSRSVTRSGLTRQTLAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 YSEILNKLYCQLAKTSLVEVLLGKDPPMGAV-LRATAIYKKTEHVAEVVRRCPHHQN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAKDAKKRKSVPTPDSTTIKKSKTASSAEEDNNEVYTLQIRGRKRYEMLK----KINDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --EDSAEHRSHLIRMEGSERAQYFEHPHTK----RQSVTVPY----EPPOLGSEFTTILL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear protein; Phosphorylation; Apoptosis.

DOMAIN 1 47 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 KFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXPRESSION (BY SIMILARITY).
SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR.
SIMILARITY: BELONGS TO THE P53 FAMILY.
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96;
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Pred. No. 1.6e-07;
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            Chordata; Cranturativati; Teleostei;
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                                                                                                                                                                       SEQUENCE FROM N.A.
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Tetraodon miurus
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367 A
                                                                                                Tetraodontidae;
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Pfam; PF00870;
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/www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
EXPRESSION (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SUBCELLULAR LOCATION: THE P53 FAMILY.
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
PHOSPHORYLATION (BY SIMILARITY).
T -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoever M., Clement J.H., Wedlich D., Montenarh M., Knoechel W., "Overexpression of wild-type p53 interferes with normal development in Xenopus laevis embryos."; Oncogene 9:109-120(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soussi T., de Fromentel C.C., Mechali M., May P., Kress M.; "Cloning and characterization of a cDNA from Xenopus laevis coding for a protein homologous to human and murine p<sup>5</sup>3."; Oncogene 1:71-78(1987).
                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00348; P53; 1.
Anti-oncogene; DNA-binding; Transcription regulation; Activator Nuclear protein; Phosphorylation; Apoptosis.
DOMAIN 1 29 TRANSCRIPTION ACTIVATION (ACIDIC).
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EMBL; M35962; AAA49923.1.

EMBL; X05191: CAA49923.1.
                                                                                                                                                                                                                                      P53)
                                                                                                                                          P07193;
01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=88143684; PubMed=2830576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94134403; PubMed=8302570;
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EMBL; X05191; CAA28821.1; -.
EMBL; X77546; CAA54672.1; -.
EMBL; S68353; AAC60746.1; -.
                                                                                                                   STANDARD;
332 DLLENKPKSKATHRPDG
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3870; P53; 1
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HSSP; P04637; 1TSR.
InterPro; IPR002117;
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                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                  Xenopodinae;
                                                                                                               P53_XENLA P07193;
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                                                                                         P53 XENLA
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collaboration
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"Nucleotide sequence of the pig p53 tumor suppressor cDNA.";

"Nucleotide sequence of the pig p53 tumor suppressor cDNA.";

Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 CTIVLYNYMCNSSCMGGMNRRPILTITLETPQGLLLGRRCFEVRVCACPGRDR-RTEED 262
                                                                                                                                                                                                                                                                                        -GGYCFSMVLDE--PPKSL- 104
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                     97
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DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
                                                                                                                                                                                                                                                                                                                                                                                                 105 WMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF--SNDVSAPVVRCQNH-LS
                                                                                                                                                                                                                                                                                                                                       38 NLSEFPDYPLAADMTVLQEGLMGNAVPTVTSCAVPSTDDYAGKYGLQLDFQQNGTAKSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 VEPLTANNAKMRESLLRSENPNSVYCGNAQGKGI----SERFSVVVPLNMSRSVTRSGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 RQTLAFKFVCQNSCIG --- RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEP--GEDAAPPSHLMRVE-----GNLQAYYMEDVNSGRHSVCVPY----EGPQVGTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 CTYSPELNKLFCQLAKTCPLLVRVESPPRGSI-LRATAVYKKSEHVAEVVKRCPHHERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL
                                                                                                                                                           Length 363;
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                                                                                                                                                                                                                         Indels
MISSING (IN REF. 2).
MISSING (IN REF. 2).
CEIF3E58F020D74D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
                                                                                                                                                        DB 1;
                                                                                                                                                                                .5e-07;
tes 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- DEPSKVRRCIAIKTEDTE 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 NYTKKRGLKPSGKRELAHPPSSEPPLPKKRLVVVDDDEE 301
                                                                                                                                                                                      ed. No. 2.5e
Mismatches
                                                                                                                                                                                                                                                                            55 NLMQFSQQSVLREMMLQDIQIQANTLPKLENHNI---
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                                                                                                                                                   8.8%; Score 176.5; 26.2%; Pred. No. 2.
                                                                                                                                                                                                              46;
                                                      40692 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPES OF CANCER.
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                        296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 LNSKKRKSVPEAAEE-
                   296
363 AA;
                                                                                                                                                                                Similarity
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                                                      SEQUENCE
                                                                                                                                                    Match
                          CONFLICT
                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                           220
                                                                                                                                                                                                                                                                                                                                                                                                                     277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326
                                                                                                                                                                SIGNAL (POTENTIAL). IMILARITY).
                                                                                                                                                                                                                                                                                                YSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF -- SNDVSAPVVRCQNHLSVEP 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKRKSVPEAAEEDEPSKVRRCIAIKTEDTESNDSRDCDDSAAEWNVSRTPDGDY-RLAIT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NDUCES
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hou E.W., Wiseman R.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANSACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -SSSPVQKKKPLDGEYFTLQIR
                                                                                                                                                                                                                                                                                                                                                        LTANNAKMRESLLRSENPNSVYCGNAQGKGISE----RFSVVVPLNMSRSVTRSGLTRQT
                                                                                                                                                                                                                                                                                                                                                                                                                LAFKFVCQNSCIG ---RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQLNS
                                                                                                                                                                                                                                                                                                                                                                                   --GNLRAEYLDDRNTFRHSVVVPY ----EPPEVGSDCTT
                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom:
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       characterization of hamster
                                                                                                                                                                                                                                                                      43;
                                                                                                            (ACIDIC)
                                                                                                                                                      DNA-BINDING)
                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                      Indels
                                                                                                        TRANSCRIPTION ACTIVATION
                                                                               regulat ton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRERFEMFRELNDALELKDAQTARESGEN--RAHSSHLKSKK 366
                                                                                                                                                  BASIC (REPRESSION O
NUCLEAR LOCALIZATIO
PHOSPHORYLATION (BY
7; A4C3D88E8DF55162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P53)
                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                    120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CPNKEWLLQSIEGMIKEAAAEVLRNPNQENLRHANKLLSLK
                                                                                                                                                                                                                                        Score 176.5; DB Pred. No. 2.7e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P53_MESAU STANDARD; PRT; 396 AA. Q00366; P97276; 01-DEC-1992 (Rel. 24, Created) 01-DEC-1992 (Rel. 24, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR
                                                                                                                                    OLIGOMERIZATION
                                                                            Transcription reation; Apoptosis
                                                                                                                                                                                                                                                                    Mismatches
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№
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MEDLINE=92210007; PubMed=1555773;
Legros Y., McIntyre P., Soussi T.;
"The cDNA cloning and immunological
Gene 112:247-250(1992).
                                                                                           Phosphorylation;
45 TRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKGQSCP----EPPPGSTKRALPTST-
                                                                                                                        BY
                                                                                                                                                                                                                                                                    49;
                                          PRINTS; PR00386; P53SUPPRESSR
PROSITE; PS00348; P53; 1.
Anti-oncogene; DNA-binding; Ti
                                                                                                                                                                                              42862 MW;
                                                                                                                                                                                                                                        8.8%;
InterPro; IPR002117; -. Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                      285
349
380
316
385
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YSDGLAP-PQHLIRVE-
                                                                                                                    94
318
361
304
385
386 AA;
                                                                                                                                                                                                                                                      Local Similarity
tes 70; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                           Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mesocricetus
                                                                                                                                                                DOMAIN
MOD_RES
SEQUENCE
                                                                                                                      DNA_BIND
                                                                                                                                                                                                                                         Query Match
                                                                                                          DOMAIN
                                                                                                                                     DOMAIN
                                                                                                                                                     DOMAIN
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253_MESAU
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                                                                                                                                                                                                                                                        Best
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                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as les concent modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                           There are no restrictions on it is as its content is in red. There are no restrictions on it is in red.
APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 EPLTANNAKMRESLLRSE-NPNSVYCGNAQGKGISERFSVVVPLNMSRSVTRSGLTRQTL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 YSIPLNKLYIRMNKAFNVDVQFKSKMP----IQPLNLRVFLCFSNDVSAPVVRCQNHLSV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --SSSPQPKRKTLDGEYFTLKIRG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
PHOSPHORYLATION (BY SIMILARITY).
G -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                  DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN MANY TYPES OF CANCER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 YSPSLNKLFCQLAKTCPVQLWVSSTPPPGTRVRAMAIYKKLQYMTEV---VRRCPHH--E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 HYNYMCNSSCMGGMNRRPILTITLEDPSGNLLGRNSFEVRICACPGRDRRTEEKNF-QK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279 KRKSVPEAAEEDEPSKVRRCIAIKTEDTESNDSRDCDDSAAEWNVSRTPDGDY-RLAITC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 AFKFVCQNSCIG --- RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQLNSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 RSSEGDGLAPPQHLIRVEGNMHAEYLDDKQ----TFRHSVVVPY----EPPEVGSDCTTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclear protein; Phosphorylation; Apoptosis.
DOMAIN 1 45 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 174; DB 1; Length 396;
Pred. No. 4.5e-07;
1; Mismatches 118; Indels
                                                                             AS AN HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     906EF02568099BE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 PNKEWLLQSIEGMIKEAAAEVLRNPNQENLRHANKLLSLK 378
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OLIGOMERIZATION.
                                                                                                                                                                                              SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                   NUCLEAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P53SUPPRESSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43631 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M75144; AAA37085.1; -. EMBL; U07182; AAB41344.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.7%;
illarity 24.9%;
Conservative 55
                                                            SUBUNIT: BINDS DNA AS SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; JH0633; JH0633.
HSSP; P04637; 1YCQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00870; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314
395
188
396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1YCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00386; PROSITE; PS00348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328
371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105
                                              EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELLULAR TUM
TP53 OR P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P53_ICTPU
093379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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punctatus (Channel catfish).

341 EWLLQSIEGMIKEAAAEVLRNPNQENLRRHANKLLS 376

316 YEFLKKINDGLE--LSDVVPPADQEKYRQ---KLLS

a

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commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                            Luft J.C., Bengten E., Clem L.W., Miller N.W., Wilson M.R.;

Tuft J.C., Bengten E., Clem L.W., Miller N.W., Wilson M.R.;

The channel catfish (Ictalurus punctatus).";

Comp. Biochem. Physiol. 120B:675-682(1998).

Comp. Biochem. Physiol. 120B:675-682(1998).

C.I. FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATE CELL DIVISION BY ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.

APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLFCQLAKTCPVLMAVSSSPPPGSV-LRATAVYKRSEHVAEVVRRCPHHERSNDSSDGPA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GGYCFSMVLDEP--PKSL-WMYSIPLN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QEVPCDVLLSDMLQPQSSSSPPTSTVPVTSDYPGLLNFTLHFQESSGTKSVTCTYSPDLN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
PHOSPHORYLATION (BY SIMILARITY).
1B89CD98DB3289F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
    Euteleostomi;
Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPGHLLRVEGNSRAVY - - - - OEDGNTQAHSVVVPYEPPQVGS(S - - - TTVLYNYMCNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF -- SNDVSAPVVRCQNHLSVEPLTANNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KMRESLLRSENPNSVYCGNAQGKGISERFSVVVPLNMSRSVTRSGLTRQTLAFKFVCQNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSVPEAAEEDEPSKVRRCIAIKTEDTESNDSRDCDDSAAEWNVSRTPDGDYRLAITCPNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -DEIYTLQVRGKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ACIDIC)
                                                                                                                                                                                                                                                                                                                               EXPRESSION (BY SIMILARITY).
SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CIG---RKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQLNSKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cion; Apoptosis.
TRANSCRIPTION ACTIVATION
BY SIMITAPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulation;
   Vertebrata; Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.6%; Score 173.5; DB 1;
larity 25.3%; Pred. No. 4.6e-07;
Conservative 57; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
OLIGOMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              randries a license agreement (see an email to license@isb-sib.ch).
Chordata; Craniata;
pterygli; Teleostei;
               Actinopterygii; Neopterygii; Teleost
Siluriformes; Ictaluridae; Ictalurus
NCBI_TaxID=7998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSVLREMMLQD-IQIQANTLPKLENHNI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear protein; Phosphorylation;
DOMAIN 1 36 TRAN
                                                                               SEQUENCE FROM N.A. MEDLINE=99071979; Pubmed=985481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002117; -. Pfam; PF00870; P53; 1. PRINTS; PR00386; P53SUPPRESSR. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF074967; AAC26824.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          989 MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00348; P53; 1. Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268
372
372
375
415
    Metazoa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 85; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303
347
286
375
376
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SEQUENCE
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Best Local (
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nasir L., Reid S.W.;

"Nucleotide sequence of exons 5 to 9 of the p53 tumour-suppressor

"Type of the horse (Equus caballus).";

"DNA Seq. 6:185-187(1996).

"I DNA Seq. 6:185-187(1996).

"I SA TUMOR SUPPRESS OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN THOM SUPPRESSION. ACTS IN CELL CYCLE REGULATION. IS A TRANS-ACTIVATED GENES TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.

APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pazzi K.A., Kraegel S.A., Griffey S.M., Theon A.P., Madewell B.R.; "Analysis of the equine tumor suppressor gene p53 in the normal horse and in eight cutaneous squamous cell carcinomas."; Cancer Lett. 107:125-130(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TUMOR TYPES. INDUCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STIMULATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription regulation; Activator;
                                            P53_HORSE STANDARD; PRT; 280 AA.
P79892; Q29481;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXPRESSION (BY SIMILARITY).
SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T -> A (IN REF. 2).
L -> M (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IN MANY TYPES OF CANCER.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97070350; PubMed=8913276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=8722575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S83123; AAB46899.1; -. U37120; AAB18936.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                            1-263 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 76-280 FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; 1.
P53; 1.
                                                                                                                                                                                                                                             Equus caballus (Horse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1SAH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96293865;
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52
276
262
79
83
                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Spleen
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                                                                                                                                                                                                                                                                                                                                                                           EQUENCE
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RESULT
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107 YSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF--SNDVSAPVVRCQNHLSVEP 164
                                                                                                                                             Gaps
                                                                                                        27;
                                                                               Length 280;
                                                                            Query Match

8.5%; Score 170.5; DB 1; Length 2
Best Local Similarity 24.8%; Pred. No. 5.5e-07;
Matches 54; Conservative 40; Mismatches 97; Indels
                                        040F12030B5ACEE9 CRC64;
A -> V (IN REF. 2).
G -> A (IN REF. 2).
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database: SPTREMBL_16:*

length: 0 length: 2000000000

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DB DB

Minimum Maximum Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

O99wzO mus musculu O88898 mus musculu Q29475 canis famil Q9jjp6 rattus norv musculu sapien sapien sapien sapien ıya arenari ıya arenari sapien sapien Q9n6d8 drosophila Q9ngc7 mya arenari Q9ngc8 mya arenari Q27937 loligo forb Q9jjp2 mus musculu O76078 homo sapien Q9nph7 homo sapien Q9up27 homo sapien Q9p1b7 homo sapien Q9h3d3 homo sapien Q9h3d3 homo sapien Q9h2d8 homo sapien Q9up28 homo sapien Q9ue10 homo sapien sapien sapien sapien loligo forb ion Descript SUMMARIES Q9N6D8 Q9NGC7 Q9NGC8 Q27937 Q9JJP2 Q9JJP2 Q9H3D2 Q9H3D3 Q9H3D3 Q9H3D3 Q9H3D4 **いらららこすすすすすすすすすす** DB Query Match Length 233.5 233.5 231.5 231.5 199.5 186 186 186 186 186 186 186 185 185 183.5 Score Result

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ALIGNMENTS

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As SUGNEME FREE S. B. Holt R.A. Evens C.A., Gocayne J.D., As Adams M.D., Celniber S.E.; Holt R.A. Evens C.A., Gocayne J.D., As Adams M.D., Celniber S.E.; Holt R.A., Evens C.A., Gocayne J.D., As Adams M.D., Celniber S.E.; Holt R.A., Evens C.A., Gocayne J.D., As Adams M.D., Celniber S.E.; Holt R.A., Evens C.G., Norther S.E.; Holt R.A., Evens C.G., Norther D.F., Tandell M.D., Zhang Q., Chen L.X., Sulton G.G., Norther D.F., Evens C.G., Helt G., Nelson C.R., Miklos G.L.G., Andrews Flannkoof C., Baldwin D., Andrews Flannkoof C., Boxen D., Box. D., Box., Mark B., Box M., Benna B. P., Bhandari D., Bolshakov S., Andrews J., Boxen M., Boxendale J., Baldwin D., Baltler H., Cadieu F., Center A., Chandra I., Boxen D. A., Boxen M., Gabriells A., Godon F., Ewill M., H., Harvis M., Gabriells M. B., Goxen M., Moren M., Gulland P., Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houte M., Allson R., Andrews M., Mourt S.M., Mourt S.M.
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larity 100.0%; Pred. No. 1.1e-168;
Conservative 0; Mismatches 0;
                                                             Proc. Natl. Acad. Sci. U.S.A. 97:7301-7306(2000).
 and Characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PR00386; P53SUPPRESSR
385 AA; 43653 MW;
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NPNSVYCGNAQGKGISERFSVVVPLNMSRSVTRSGLTRQTLAFKFVCQNSCIGRKETSLV
                                                                   FCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQLNSKKRKSVPEAAEEDEPSKVRRCIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metazoa; Mollusca; Bivalvia; Heteroconchia; Myoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kelley M.L., Heaney J.D., Winge P., Van Beneden R.J., Walker C "Conserved p53/p73 homologs are differentially expressed in a naturally occurring invertebrate leukemia.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF253324; AAF67734.1;
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69244 MW; AB1F0C66E0010AED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  Last annotation update)
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                                                                                                                                                                                                                                                                                                                              PRT;
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2001 (TrEMBLrel. 16,
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InterPro; IPR002117;
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Pfam; PF00870; P53;
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PRINTS; PR00386;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 NOPMSOETFEYLWHTLEEVTDNVDYTHINTRELDYSYDDSE----DGTSLQVEKFRINQH 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 VLGRRCVEVRICACPGRDRKADERGSLPPMVSGGVKKSQMPKFSMGTEITTVSSGKKRKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -ODICIOANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QPLNLRVFLCF - - SNDVSAPVVRCQNHLSVEPLTANNAKMRESLLRSENPNSVYCGNAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTDVSDLLNPIIGTTSSSSMSPDSQTNISGSTASSPYQEMALTSPPPYSPHTNLTSPIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 PGCVIRSMPIFMKPEHVQEAVKRCPNHATSKEFNENHPAPNH-I,VRCEHKVSKYVEDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVGQHVIHVKICTCPKRDRIQDER-----QLNSKKRKSVPEAAEEDEPSKVRRCIAI
                                                                                                                                                                                                                                                                                                                                                                                                                          ----WH--KESTDSED----DSTEVDIKEDIPKTVEVSGSELTTEPMAFL
                                                                                                                                                                                                                                                                                                                                                                                                   77;
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                                                                                                                                                                 Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Myoida;
                                                                                                                                                                                                                                                       Ø
                                                                                                                                                                                                                                    Kelley M.L., Heaney J.D., Winge P., Van Beneden R.J., Walker "Conserved p53/p73 homologs are differentially expressed in naturally occurring invertebrate leukemia.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF253323; AAF67733.1; -.
InterPro; IPR002117; -.
Pfam; PF00870; P53; 1.
PFam; PF008870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
SEQUENCE 443 AA; 50177 MW; 506E11FAAE719F68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
P53 TUMOR SUPPRESSOR HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --SVLREMML--
                                                                                                                                 epdn
                                                                                                                                                                                                                                                                                                                                                                         Score 231.5; DB 5;
Pred. No. 2.9e-12;
3; Mismatches 140;
                                                                                                                   update
                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-MAR-2001 (TrEMBLrel. 16, Last annotation
P53 TUMOR SUPPRESSOR-LIKE PROTEIN.
Mya arenaria.
                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                  48;
                                                                                                                                                                                                                                                                                                                                                                         11.5%;
illarity 27.2%;
Conservative 4
                                                                                 PRELIMINARY;
                                                                                                                                                                            Myoidea; Myidae; Mya.
NCBI_TaxID=6604;
                                                                                                                                                                                                                                                                                                                                                                                       . Similarity 99; Conser
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                     366
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304 EDTE
                      EDDE
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Q27937;
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235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yang A., Walker N., Bronson R., Kaghad M., Oosterwegel M., Bonnin ...
Vagner C., Bonnet H., Dikkes P., Sharpe A., McKeon F., Caput D.;
"p73-deficient mice have neurological, pheromonal and inflammatory defects but lack spontaneous tumors.";
Nature 404:99-103(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IYMK----PEHVQEVVKRCPNHATAK---EHNEKHPAPLHIVRCEHKLAKY----HEDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 LNLRVFLCFSNDVSAPVVRCQNHLSVEPLTANNAKMRESL--LRSENPNSVYCGNAQGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 ISERFSVVVPLNMSRSVTRSGLTRQTLAFKFVCQNSCIG---RKETSLVFCLEKACGDIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 GQHVIHVKICTCPKRDRIQDER-QLNSK----KRKSVPEAA-----EEDEPSKVR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Loligo forbesi (Northern European squid).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Teuthoida;
Myopsida; Loliginidae; Loligo.
NCBI_TaxID=6618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                SEQUENCE FROM N.A.
TISSUE=OPTIC LOBE;
Winge P., Friend S., Fleming J.T.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
EMBL; U43595; AAA98563.1; -.
EMBL; U43596; AAA98564.1; -.
HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 GGYCFSMVLDEPPK----SLWMYSIPLNKLYIRMNKAFNVDVQFKSKMP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                               C4B41AFC94F0EFFB CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 RCIAIKTEDTESND----SRDCDDSAAEWNVSRTPDGD 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 209; DB 5;
Pred. No. 3.8e-10
1; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351 ECFTLKVRGRENYEILCKLRDIMELAA----RIPEAE
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MEDLINE=20179195; PubMed=10716451;
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                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; -; 1. SMART; SM00454; SAM; 1. SEQUENCE 564 AA; 63873 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.4%; 28.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAB81953.1; -.
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. P73 ALPHA PROTEIN.
                                                                                                                                                                                                                                                                                       InterPro; IPR001660; -InterPro; IPR002117; -Pfam; PF00536; SAM; 1. Pfam; PF00870; P53; 1.
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nes 79; Conserv
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                                                                                                                                       S 103
                                                                          Gaps
                                                                                              58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98448095; PubMed=9774969; Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C Caput D., McKeon F.; "p63, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities."; Mol. Cell 2:305-316(1998).
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                                                                                                                                                                              LWMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQP-LNLRVFLCF--SNDVSAPVVRCQNHL
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                                                                                                                                                    HFEVTFQQSSTAKSA
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                                                                                                         TWIYSPLLKKLYCQIAK - - TCPIQIKVSTPPPPGTAIRAMPVYKKAEHVTDIVKRCPNF
                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human lung cancer.";
                                                                                                                                       4-- pp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa
Yokota J.;
                                                     631;
                                                                          63,
                                                                                                                                                                                                                                                                 TLAFKFVCQNSCIG ---RKETSLVFCLERACGDIVGQHVIHVKICTCPKRDRIQDE
                                                                                                                                     CFSMVLDE-
                                                     Length
                                                                          Indels
PD002681; -; 1.
PS00348; P53; UNKNOWN_1.
: 631 AA; 69095 MW; E364D566A90CBF1D CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                update)
on update)
                                                                                                                                                           19---
                                                     DB 11;
                                                                                                                                     -FSQQSVLREMMLQDIQIQANT-LPKLENHNIG
                                                                        128;
                                                                                              EDDSTEVDIKEDIPKTVEVSGSELTTEPMAFLQCLNSGNLMQ-
                                                    Score 199.5; D
Pred. No. 3e-09
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(TrEMBLrel. 08, Last sequence up
(TrEMBLrel. 16, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene in
                                                                         Mismatches
                                                                                                                                                    EHAASAPTHSPYAQPSSTFDTMSPAPVIPSNTDYP-
                                                                                                                                                                                                                                                                                                                                                                                448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=SKELETAL MUSCLE;
MEDLINE=98324755; PubMed=9662378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                       42;
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EMBL; AF075428; AAC62633.1; EMBL; AB016072; BAA32592.1; EMBL; AF116770; AAF43486.1; ---
                                                    9.9%;
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                             314
                                                              Local Similarity
Les 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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01-NOV-1998
01-MAR-2001
 Prodom; P
PROSITE;
SEQUENCE
                                                    Query Match
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256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGYCFSMVLDE---PPKSLWMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SNDVSAPVVRCQNHLSVEPLTANNAKMRESLLRSENPNSVYCGNAQGKGISE----RF
                                                                                                                                                                                                                                                                                                                                                                                                                ---WPQYTNLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVVVPLNMSRSVTRSGLTRQTLAFKFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 SVLVPY----EPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- GNSHAQYVEDPITGRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP-QGAVIRAMPVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20388515; PubMed=10935472;
Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa
                                                                                                                                                                                                                                                                                                                                         80;
                                                                                                                                                                                                                                                                                                       DB 4; Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Mutation and expression of the p51 gene in human lung car

Neoplasia 1:71-79(1999).

EMBL; AF116771; AAF61624.1; -.

EMBL; AF116769; AAF43489.1; -.

EMBL; AF116757; AAF43489.1; JOINED.

EMBL; AF116757; AAF43489.1; JOINED.

EMBL; AF116760; AAF43489.1; JOINED.

EMBL; AF116761; AAF43489.1; JOINED.

EMBL; AF116761; AAF43489.1; JOINED.
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                  A4FF56B8D1E7B3A6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                         124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 EARICACPGRDRKADE---DSIRKQQVSDSTKNGDGTK 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.3%; Score 186; DB 4 22.2%; Pred. No. 3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 HVKICTCPKRDRIQDERQLNSKKRKSVPEAAEEDEPSK
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Mismatches
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Eutheria; Primates; Catarrhini;
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                                                                                                                                                                          InterPro; IPR002117; -. Pfam; PF00870; P53; 1. PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; -; 1. SEQUENCE 448 AA; 50951 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 15, (TrEMBLrel. 15, 1 (TrEMBLrel. 16, 1
AAF43486.1;
AAF43486.1;
AAF43486.1;
AAF43486.1;
AAF43486.1;
AAF43486.1;
AAF43486.1;
AAF43486.1;
AAF43486.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISOFORM TAP63DELTA (P51
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                       IPR002117;
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                          IXCS
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                                                                AF116761;
AF116762;
AF116763;
AF116764;
AF116756;
AF116757;
AF116759;
AF116760;
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                                                                                                                                         AF116765;
P04637; 1Y
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01-MAR-2001
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01-0CT-2000
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Yokota J.;
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Mon

86CC865BDF2643DD CRC64;

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487 AA; 55687 MW;
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                                                             75;
        SEQUENCE
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                                                                                                                                                                                                                                                                             CF 145
                                                                                                                                                                                                                                                                                                                           RF 199
                                                                                                                                                                                                                                                                                                                                                                         SVVVPLNMSRSVTRSGLTRQTLAFKFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVI 256
                                                                                                                                                            Gaps
                                                                                                                                                                                   63
                                                                                                                                                                                                         -WPQYTNLG 76
                                                                                                                                                                                                                               NI 88
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                                                                                                                                                                                                                                                                                                                                                   -GNSHAQYVEDPITGRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                               OPMSWHKESTDSEDDST-EVDIKEDIPKTVEVSGSELTTEPMAFLQGLNSGNLMQFSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98448095; PubMed=9774969; Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V Andrews N.C., Caput D., McKeon F.; "p63, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities Mol. Cell 2:305-316(1998).
                                                                                                                                                                                                                                                                             --PPKSLWMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFL
                                                                                                                                                           80;
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF124540; AAG45609.1; --
EMBL; AF124528; AAG45609.1; JOINED.
EMBL; AF124531; AAG45609.1; JOINED.
EMBL; AF124532; AAG45609.1; JOINED.
EMBL; AF124533; AAG45609.1; JOINED.
EMBL; AF124533; AAG45609.1; JOINED.
EMBL; AF124535; AAG45609.1; JOINED.
                                                                                                                                                          Indels
EMBL; AF116763; AAF43489.1; JOINED.
EMBL; AF116764; AAF43489.1; JOINED.
EMBL, AF116765; AAF43489.1; JOINED.
EMBL, AF116766; AAF43489.1; JOINED.
InterPro; IPR002117; -.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
PROSITE; PS00348; P53; UNKNOWN_1.
SEQUENCE 471 AA; 52882 MW; 32EB39798FC1CE69 CRC64
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Catarrhini; Hominidae;
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Last annotation updat
                                                                                                                                                          124;
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                                                                                                                               Score 186; DB 4;
Pred. No. 3.2e-08;
9; Mismatches 124,
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                                                                                                                                                                                                                               --ANTLPKLENH-
                                                                                                                                                        59;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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01-MAR-2001 (TrEMBLrel
01-MAR-2001 (TrEMBLrel
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SEQUENCE FROM N.A
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15;
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                                                                                                                                                                                                                                                                                                                                                                                                           --SNDVSAPVVRCQNHLSVEPLTANNAKMRESLLRSENPNSVYCGNAQGKGISE----RF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVVVPLNMSRSVTRSGLTRQTLAFKFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVI 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 SVLVPY----EPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCF 340
                                                                                                                                                      --WPQYTNLG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 LLNSM---DQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYP 133
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V., Andrews N.C., Caput D., McKeon F.; "p63, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities."; Mol. Cell 2:305-316(1998).

EMBL; AF075432; AAC62637.1; -.

HSSP; P04637; 1YCS.

InterPro; IPR002117; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               232 KKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVE-----GNSHAQYVEDPITGRQ
                                                                                                                                                                                                                                                                                                                                          173 GPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP-QGAVIRAMPVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                       80;
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     Length 487;
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                                                    Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                            70 QPIDLNFVDEPSEDGATNKIEISMD---CIRMQDSDL-SDPM--
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9.3%; Score 186; DB 4; 22.2%; Pred, No. 3.3e-08;
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Mismatches
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MEDLINE=98448095; PubMed=9774969;
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PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; -; 1.
SEQUENCE 516 AA; 57697 MW;
                                                  Conservative
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                      Similarity
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193 KKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVE-----GNSHAQYVEDPITGRQ
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                                                                                                                                    F 301
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                 -RF
                                                                             -GNSHAQYVEDPITGRQ
  [±4
                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GGYCFSMVLDE---PPKSLWMYSIPLNKLYIRINKAFNVDVQFKSKMPIQPLNLRVFLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            the p51 gene in human lung cancer.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                   O., Ikawa
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                                                  --SNDVSAPVVRCQNHLSVEPLTANNAKMRESLLRSENPNSVYCGNAQGKGISE
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Ishimoto
                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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Pred. No. 3.5e-08;
9; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07553781103738B1
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                                                                                                                                                             257 HVKICTCPKRDRIQDERQLNSKKRKSVPEAAEEDEPSK
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                                                                   C., Kohno
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                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=10935472;
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PROSITE; PS00348; P53; UNKNOWN_1
SEOUENCE 516 AA; 57598 MW; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawahara
                                                                                                                                                                                                                                                                                 (TrEMBLrel. 15, C) (TrEMBLrel. 15, I) (TrEMBLrel. 16, I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mutation and expression of Neoplasia 1:71-79(1999).

EMBL; AF116756; AAF43488.1; EMBL; AF116757; AAF43488.1; EMBL; AF116757; AAF43488.1; EMBL; AF116760; AAF43488.1; EMBL; AF116761; AAF43488.1; EMBL; AF116762; AAF43488.1; EMBL; AF116765; AAF43488.1; EMBL; AF116765; AAF43488.1; EMBL; AF116766; AAF43488.1; EMBL; AF116766; AAF43488.1; EMBL; AF116766; AAF43488.1;
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                                                                                                                                                                                                                                                                                                                                        (Human)
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Best Local Similarity
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1870; P53;
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01-OCT-2000
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Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
Andrews N.C., Caput D., McKeon F.;
"p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998).
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SVVVPLNMSRSVTRSGLTRQTLAFKFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVI
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF124528; AAG45608.1; -.
EMBL; AF124529; AAG45608.1; JOINED.
EMBL; AF124529; AAG45608.1; JOINED.
EMBL; AF124531; AAG45608.1; JOINED.
EMBL; AF124533; AAG45608.1; JOINED.
EMBL; AF124534; AAG45608.1; JOINED.
EMBL; AF124535; AAG45608.1; JOINED.
EMBL; AF124535; AAG45608.1; JOINED.
EMBL; AF124535; AAG45608.1; JOINED.
EMBL; AF124537; AAG45608.1; JOINED.
EMBL; AF124537; AAG45608.1; JOINED.
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Last annotation update)
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Pred. No. 3.9e-08;
9; Mismatches 124;
                                                                                                                                                                                                                                                                                        302 EARICACPGRDRKADE---DSIRKQQVSDSTKNGDGTK 336
                                                                                                                                                                                                                            257 HVKICTCPKRDRIQDERQLNSKKRKSVPEAAEEDEPSK 294
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Best Local Similarity 22.2%; Pr
Matches 75; Conservative 59;
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| (TrEMBLrel. 16, 0
| (TrEMBLrel. 16, 0
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01-MAR-2001
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PRELIMINARY;
      Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLNSM---DQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NI 88
                                                                                                                                                                                                                                        Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V., Andrews N.C., Caput D., McKeon F.; "p63, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities."; Mol. Cell 2:305-316(1998).

EMBL; AF075430; AAC62635.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QPMSWHKESTDSEDDST-EVDIKEDIPKTVEVSGSELTTEPMAFLQGLNSGNLMQFSQQS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 KKAEHVTEVVKRCPNHELSREFNEGOIAPFOHLIRVE-----GNSHAQYVEDPITGRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --WPOYTNLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGYCFSMVLDE---PPKSLWMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --SNDVSAPVVRCQNHLSVEPLTANNAKMRESLLRSENPNSVYCGNAQGKGISE--
                                                                                                                                                                                                                                                                                                                                                                                                                              641;
                                                                                                                                                                                    Homo
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                                                                                                                                                                                                                                                                                                                                                                                       23A2E5EBAE63F605 CRC64;
                                                                                                                                                               Eutheria; Primates; Craniata; Vertebrata; | Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 16, Last annotation update)
P51 ISOFORM TAP63ALPHA (P51B PROTEIN).
HOMO Sapiens (Human).
                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 186; DB 4;
Pred. No. 4.7e-08;
); Mismatches 124
257 HVKICTCPKRDRIQDERQLNSKKRKSVPEAAEEDEPSK
             :|| || || || || 341 EARICACPGRDRKADE---DSIRKQQVSDSTKNGDGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HVKICTCPKRDRIQDERQLNSKKRKSVPEAAEEDEPSK
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                                                                                                           Created)
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                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=98448095; PubMed=9774969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLREMMLQDIQIQ - - - ANTLPKLENH -
                                                                                                                                                                                                                                                                                                                          InterPro; IPR001660; -.
InterPro; IPR002117; -.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
SMART; SM00454; SAM; 1.
SEQUENCE 641 AA; 72049 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   59;
                                                                                                                                                                                                                                                                                                                                                                       , SAM; 1.
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13,
16,
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                                                                                   PRELIMINARY;
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                                                                                          09UP28;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
TA P63 ALPHA.
                                                                                                                                                        Homo sapiens (Human)
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Best Local Similarity
                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                    Eukaryota;
Mammalia;
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075195;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP-QGAVIRAMPVY 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 KKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVE-----GNSHAQYVEDPITGRQ 245
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                                                                                                                                                                                                                                                             Osada M., Obba M., Kawahara C., Ishioka C., Kanamaru R., Katoh I., Ikawa Y., Nimura Y., Nakagawara A., Obinata M.; "Cloning and functional analysis of human p51, which structurally functionally resembles p53."; Nat. Med. 4:839-844(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGYCFSMVLDE---PPKSLWMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFLCF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --SNDVSAPVVRCQNHLSVEPLTANNAKMRESLLRSENPNSVYCGNAQGKGISE----RF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -WPOYTNLG
Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 SVVVPLNMSRSVTRSGLTRQTLAFKFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the p51 gene in human lung cancer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa
Yokota J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80;
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                                      Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 186; DB 4;
Pred. No. 4.7e-08;
9; Mismatches 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 EARICACPGRDRKADE---DSIRKQQVSDSTKNGDGTK 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 HVKICTCPKRDRIQDERQLNSKKRKSVPEAAEEDEPSK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  680 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOINED
                                                                                                                                                                                   TISSUE=SKELETAL MUSCLE;
MEDLINE=98324755; PubMed=9662378;
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. 72019 MW;
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PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mutation and expression of the Neoplasia 1:71-79(1999).
EMBL; AB016073; BAA32593.1; EMBL; AF116769; AAF43487.1; GEMBL; AF116756; AAF43487.1; JUEMBL; AF116759; AAF43487.1; JUEMBL; AF116760; AAF43487.1; JUEMBL; AF116761; AAF43487.1; JUEMBL; AF116763; AAF43487.1; JUEMBL; AF116764; AAF43487.1; JUEMBL; AAF43487.1; JUEMBL; AAFA3487.1; JUEM
                                             Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.38;
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AAF43487.1;
AAF43487.1;
AAF43487.1;
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                                  Eutheria;
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Best Local Similarity
                                                                                                                                                       SEQUENCE FROM N.A
                                    Mammalia; Euther NCBI_TaxID=9606;
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AF116763;
AF116764;
AF116765;
AF116766;
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Search completed: November 16, 2001, 15:58:09
Job time: 496 sec
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                                                                                                                                                                                  16.";
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                    QPMSWHKESTDSEDDST-EVDIKEDIPKTVEVSGSELTTEPMA-LQGLNSGNLMQFSQQS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                     88
                                                                                                                      SEQUENCE FROM N.A.

TISSUE=SKELETAL MUSCLE AND KERATINOCYTE CULTURE;

MEDLINE=99018225; PubMed=9799841;

Augustin M., Bamberger C., Paul D., Schmale H.;

"Cloning and chromosomal mapping of the human p53-related KET gene chromosome 3q27 and its murine homolog Ket to mouse chromosome 16.

Mamm. Genome 9:899-902(1998).

REMBL; Y16961; CAA76562.1; -.

REMBL; P04637; 1YCS.

InterPro; IPR001660; -.

RICHARDOLLORES INTERVALUES.

InterPro; IPR00117; -.
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TLETRDGQVLGRRCF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGYCFSMVLDE---PPKSLWMYSIPLNKLYIRMNKAFNVDVQFKSKMPIQPLNLRVFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVM?PPP-QGAVIRAMP
                                                                                                                                                                                                                                                                                                                                                                                                              -- WPQYTN
                                                                              Euteleostom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --SNDVSAPVVRCQNHLSVEPLTANNAKMRESLLRSENPNSVYCGNAQGKGISE-
                                                                                                                                                                                                                                                                                                                                         Length 680;
                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                     6548A6F2187D852E CRC64;
                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update;
Last annotation update)
                                                                                                                                                                                                                                                                                                                                     9.3%; Score 186; DB 4; larity 22.2%; Pred. No. 5e-08; Conservative 59; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVLVPY----EPPQVGTEFTTVLYNFMCNSSCVGGMNRRPIL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVE----
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                                                                                                                                                                                                                                                                                                                                                                                                  ||: : ||| :| |:| |:| | OPIDLNFVDEPSEDGATNKIEISMD---CIRMQDSDL-SDPM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 HVKICTCPKRDRIQDERQLNSKKRKSVPEAAEEDEPSK
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         Created)
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                                                                                                                                                                                                                                                                  P53SUPPRESSR
                                                                                                                                                                                                                                                                                                    76776 MW;
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       13,
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       (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                        SAM;
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                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                     Pfam; PF00870; P53;
                                                                                                                                                                                                                                                               PRINTS; PR00386; P. ProDom; PD002681; SMART; SM00454; SA
                                                                                                                                                                                                                                                                                                    680 AA;
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                                                                                                  NCBI_TaxID=9606;
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      01.-MAY-2000
01-MAY-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9H3D4;
01-MAR-2001
01-MAR-2001
01-MAR-2001
                                          KET PROTEIN
                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --SNDVSAPVVRCQNHLSVEPLTANNAKMRESLLRSENPNSVYCGNAQGKGISE----RF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --WPQYTNLG 115
MEDLINE=98448095; PubMed=9774969;
Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
Andrews N.C., Caput D., McKeon F.;
"p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 GPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP-QGAVIRAMPVY
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                                                                                                                                                                                                                                         Hagiwara K., McMenamin M.G., Harris C.C.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF124539; AAG45607.1; JOINED.
EMBL; AF124529; AAG45607.1; JOINED.
EMBL; AF124531; AAG45607.1; JOINED.
EMBL; AF124532; AAG45607.1; JOINED.
EMBL; AF124533; AAG45607.1; JOINED.
EMBL; AF124533; AAG45607.1; JOINED.
EMBL; AF124534; AAG45607.1; JOINED.
EMBL; AF124535; AAG45607.1; JOINED.
EMBL; AF124536; AAG45607.1; JOINED.
EMBL; AF124538; AAG45607.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341 EARICACPGRDRKADE---DSIRKQOVSDSTKNGDGTK 375
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